```
AGC TCC ACC GCG GTG GCG GCC GCT CTA GAA CTA GTG GAT CCC CCG GGC      48
Ser Ser Thr Ala Val Ala Ala Ala Leu Glu Leu Val Asp Pro Pro Gly

TGC AGG AAT TCG GCA CGA GCC GAT CTC GGT GCC GAC CGC CTC TCC AAG      96
Cys Arg Asn Ser Ala Arg Ala Asp Leu Gly Ala Asp Arg Leu Ser Lys

ATC GAC AAG GAG AGA GCC GGA GTG CTG GTC GGA ACA GGA ATG GGT GGT     144
Ile Asp Lys Glu Arg Ala Gly Val Leu Val Gly Thr Gly Met Gly Gly

CTG ACT GTC TTC TCT GAC GGG GTT CAG TCT CTT ATC GAG AAG GGT CAC     192
Leu Thr Val Phe Ser Asp Gly Val Gln Ser Leu Ile Glu Lys Gly His

CGG AAA ATC ACC CCT TTC TTC ATC CCC TAT GCC ATT ACA AAC ATG GGG     240
Arg Lys Ile Thr Pro Phe Phe Ile Pro Tyr Ala Ile Thr Asn Met Gly

TCT GCC CTG CTC GCT ATC GAA TTT GGT CTC ATG GGC CCA AAC TAT TCA     288
Ser Ala Leu Leu Ala Ile Glu Phe Gly Leu Met Gly Pro Asn Tyr Ser

ATT TCC ACT GCA TGT GCC ACT TCC AAC TAC TGC TTC CAT GCT GCC GCT     336
Ile Ser Thr Ala Cys Ala Thr Ser Asn Tyr Cys Phe His Ala Ala Ala

AAT CAT ATC CGC CGT GGT GAG GCT GAT CTT ATG ATT GCT GGA GGC ACT     384
Asn His Ile Arg Arg Gly Glu Ala Asp Leu Met Ile Ala Gly Gly Thr
```

FIGURE 1

```
GAG GCC GCA ATC ATT CCA ATT GGG TTG GGA GGC TTT GTG GCT TGC AGG      432
Glu Ala Ala Ile Ile Pro Ile Gly Leu Gly Gly Phe Val Ala Cys Arg

GCT TTG TCT CAA AGG AAC GAT GAC CCG CAG ACT GCC TCT AGG CCC TGG      480
Ala Leu Ser Gln Arg Asn Asp Asp Pro Gln Thr Ala Ser Arg Pro Trp

GAT AAA GAC CGT GAT GGT TTT GTG ATG GGT GAA GGT GCT GGA GTG TTG      528
Asp Lys Asp Arg Asp Gly Phe Val Met Gly Glu Gly Ala Gly Val Leu

GTG ATG GAG AGC TTG GAA CAT GCA ATG AGA CGA GGA GCA CCG ATT ATT      576
Val Met Glu Ser Leu Glu His Ala Met Arg Arg Gly Ala Pro Ile Ile

GCA GAG TAT TTG GGA GGT GCA ATC AAC TGT GAT GCT TAT CAC ATG ACT      624
Ala Glu Tyr Leu Gly Gly Ala Ile Asn Cys Asp Ala Tyr His Met Thr

GAT CCA AGG GCT GAT GGT CTT GGT GTC TCT TCT TGC ATT GAG AGT AGC      672
Asp Pro Arg Ala Asp Gly Leu Gly Val Ser Ser Cys Ile Glu Ser Ser

CTT GAA GAT GCT GGC GTC TCA CCT GAA GAG GTC AAT TAC ATA AAT GCT      720
Leu Glu Asp Ala Gly Val Ser Pro Glu Glu Val Asn Tyr Ile Asn Ala
```

FIGURE 1

```
CAT GCG ACT TCT ACT CTA GCT GGG GAT CTC GCC GAG ATA AAT GCC ATC      768
His Ala Thr Ser Thr Leu Ala Gly Asp Leu Ala Glu Ile Asn Ala Ile

AAG AAG GTT TTC AAG AAC ACA AAG GAT ATC AAA ATT AAT GCA ACT AAG      816
Lys Lys Val Phe Lys Asn Thr Lys Asp Ile Lys Ile Asn Ala Thr Lys

TCA ATG ATC GGA CAC TGT CTT GGA GCA TCT GGA GGT CTT GAA GCT ATA      864
Ser Met Ile Gly His Cys Leu Gly Ala Ser Gly Gly Leu Glu Ala Ile

GCG ACT ATT AAG GGA ATA AAC ACC GGC TGG CTT CAT CCC AGC ATT AAT      912
Ala Thr Ile Lys Gly Ile Asn Thr Gly Trp Leu His Pro Ser Ile Asn

CAA TTC AAT CCT GAG CCA TCG GTG GAG TTC GAC ACT GTT GCC AAC AAG      960
Gln Phe Asn Pro Glu Pro Ser Val Glu Phe Asp Thr Val Ala Asn Lys

AAG CAG CAA CAC GAA GTT AAC GTT GCG ATC TCG AAT TCA TTC GGA TTT     1008
Lys Gln Gln His Glu Val Asn Val Ala Ile Ser Asn Ser Phe Gly Phe

GGA GGC CAC AAC TCA GTC GTG GCT TTC TCG GCT TTC AAG CCA TGATTA      1056
Gly Gly His Asn Ser Val Val Ala Phe Ser Ala Phe Lys Pro
```

FIGURE 1

CCCATTTCAC AAGGTACTTG TCATTGAGAA TACGGATTAT GGACTTGCAG AGTAATTTCC 1116

CCATGTTTGT CGGAAGAGCA TATTACCACG GTTGTCCGTC AAACCCATTT AGGATACTGT 1176

TCTATGTAAT AAAACTAAGG ATTATTTAAT TCCCTTTTTA TCCTGTCTCC AGTTTGAGCA 1236

TGAAATTATA TTTATTTTTA CTTAGAAAGG TCAAATAAGA TTTTGTTTTA CCTCTGTAAA 1296

ACTTTTGTTT GTATTGGAAA GGAAGTGCCG TCTCAAAAAA AAAAAAAAAA AA 1348

FIGURE 1

Sequence Range: 1 to 1704

```
                          10          20          30          40
AAA TTA ACC CTC ACT AAA GGG AAC AAA AGC TGG AGC TCC ACC GNG GTG
Lys Leu Thr Leu Thr Lys Gly Asn Lys Ser Trp Ser Ser Thr Xxx Val>

50          60          70          80          90
            *
GCG GCC GCT CTA GAA CTA GTG GAT CCC CCG GGC TGC AGG AAT TCG GCA
Ala Ala Ala Leu Glu Leu Val Asp Pro Pro Gly Cys Arg Asn Ser Ala>

  100         110         120         130         140
                          *
CGA GCC GGC ATG GGC CTC GTC TCC GTA TTC GGC TCC GAC GTC GAC TCT
Arg Ala Gly Met Gly Leu Val Ser Val Phe Gly Ser Asp Val Asp Ser>

    150         160         170         180         190
                                        *
TAT TAC GAA AAG CTC CTC TCC GGC GAG AGC GGG ATC AGC TTA ATC GAC
Tyr Tyr Glu Lys Leu Leu Ser Gly Glu Ser Gly Ile Ser Leu Ile Asp>

       200         210         220         230         240
                                                       *
CGC TTC GAC GCT TCC AAG TTC CCC ACC AGG TTC GGC GGC CAG ATC CGG
Arg Phe Asp Ala Ser Lys Phe Pro Thr Arg Phe Gly Gly Gln Ile Arg>

          250         260         270         280
GGA TTC AAC GCG ACG GGA TAC ATC GAC GGG AAG AAC GAC AGG AGG CTC
Gly Phe Asn Ala Thr Gly Tyr Ile Asp Gly Lys Asn Asp Arg Arg Leu>

90          300         310         320         330
            *
GAC GAT TGC CTC CGC TAC TGC ATT GTC GCC GGG AAG AAG GCT CTC GAA
Asp Asp Cys Leu Arg Tyr Cys Ile Val Ala Gly Lys Lys Ala Leu Glu>
```

FIGURE 2

```
  340          350          360          370          380
                             *
AAT TCC GAT CTC GGC GGT GAA AGC CTC TCC AAG ATT GAT AAG GAG AGA
Asn Ser Asp Leu Gly Gly Glu Ser Leu Ser Lys Ile Asp Lys Glu Arg>

    390          400          410          420          430
                                           *
GCT GGA GTG CTA GTT GGA ACT GGT ATG GGT GGC CTA ACC GTC TTC TCT
Ala Gly Val Leu Val Gly Thr Gly Met Gly Gly Leu Thr Val Phe Ser>

       440          450          460          470          480
                                                             *
GAC GGG GTT CAG AAT CTC ATC GAG AAA GGT CAC CGG AAG ATC TCC CCG
Asp Gly Val Gln Asn Leu Ile Glu Lys Gly His Arg Lys Ile Ser Pro>

          490          500          510          520
TTT TTC ATT CCC TAT GCC ATT ACA AAC ATG GGG TCT GCT CTG CTT GCC
Phe Phe Ile Pro Tyr Ala Ile Thr Asn Met Gly Ser Ala Leu Leu Ala>

30        540          550          560          570
                *
ATC GAT TTG GGT CTG ATG GGC CCA AAC TAT TCG ATT TCA ACT GCA TGT
Ile Asp Leu Gly Leu Met Gly Pro Asn Tyr Ser Ile Ser Thr Ala Cys>

  580          590          600          610          620
                             *
GCT ACT TCC AAC TAC TGC TTT TAT GCC GCT GCC AAT CAT ATC CGC CGA
Ala Thr Ser Asn Tyr Cys Phe Tyr Ala Ala Ala Asn His Ile Arg Arg>

    630          640          650          660          670
                                           *
GGC GAG GCT GAC CTC ATG ATT GCT GGA GGA ACT GAG GCT GCA ATC ATT
Gly Glu Ala Asp Leu Met Ile Ala Gly Gly Thr Glu Ala Ala Ile Ile>
```

FIGURE 2

```
       680          690          700          710          720
CCA ATT GGG TTA GGA GGA TTC GTT GCC TGC AGG GCT TTA TCT CAA AGG
Pro Ile Gly Leu Gly Gly Phe Val Ala Cys Arg Ala Leu Ser Gln Arg>

          730          740          750          760
AAT GAT GAC CCT CAG ACT GCC TCA AGG CCG TGG GAT AAG GAC CGT GAT
Asn Asp Asp Pro Gln Thr Ala Ser Arg Pro Trp Asp Lys Asp Arg Asp>

70          780          790          800          810
GGT TTT GTG ATG GCC GAA GGG GCT GGA GTA TTG GTT ATG GAG AGC TTG
Gly Phe Val Met Gly Glu Gly Ala Gly Val Leu Val Met Glu Ser Leu>

  820          830          840          850          860
GAA CAT GCA ATG AAA CGA GGA GCG CCG ATT ATT GCA GAA TAT TTG GGA
Glu His Ala Met Lys Arg Gly Ala Pro Ile Ile Ala Glu Tyr Leu Gly>

    870          880          890          900          910
GGT GCA GTC AAT TGT GAT GCT TAT CAT ATG ACT GAT CCA AGG GCT GAT
Gly Ala Val Asn Cys Asp Ala Tyr His Met Thr Asp Pro Arg Ala Asp>

       920          930          940          950          960
GGG CTT GGT GTC TCC TCT TGC ATT GAG AGC AGT CTG GAA GAT GCT GGG
Gly Leu Gly Val Ser Ser Cys Ile Glu Ser Ser Leu Glu Asp Ala Gly>

          970          980          990          1000
GTC TCA CCT GAA GAG GTC AAT TAC ATA AAT GCT CAT GCG ACT TCC ACT
Val Ser Pro Glu Glu Val Asn Tyr Ile Asn Ala His Ala Thr Ser Thr>
```

FIGURE 2

```
10          1020          1030          1040          1050
CTT GCT GGG GAT CTT GCC GAG ATA AAT GCC ATC AAG AAG GTT TTC AAG
Leu Ala Gly Asp Leu Ala Glu Ile Asn Ala Ile Lys Lys Val Phe Lys>

 1060          1070          1080          1090          1100
AAC ACC AAG GAA ATC ACA ATC AAT GCA ACT AAG TCG ATG ATC GGA CAC
Asn Thr Lys Glu Ile Thr Ile Asn Ala Thr Lys Ser Met Ile Gly His>

   1110          1120          1130          1140          1150
TGT CTT GGA GCA TCA GGG GGT CTT GAA GCC ATT GCG ACA ATT AAG GGA
Cys Leu Gly Ala Ser Gly Gly Leu Glu Ala Ile Ala Thr Ile Lys Gly>

      1160          1170          1180          1190          1200
ATA ACC ACC GGC TGG CTT CAT CCC AGC ATA AAC CAA TTC AAT CCC GAG
Ile Thr Thr Gly Trp Leu His Pro Ser Ile Asn Gln Phe Asn Pro Glu>

         1210          1220          1230          1240
CCA TCA GTG GAA TTC GAC ACA GTT GCC AAC AAG AAG CAG CAA CAT GAA
Pro Ser Val Glu Phe Asp Thr Val Ala Asn Lys Lys Gln Gln His Glu>

50          1260          1270          1280          1290
GTG AAT GTT GCT ATC TCA AAT TCA TTC GGA TTC GGA GGC CAC AAC TCA
Val Asn Val Ala Ile Ser Asn Ser Phe Gly Phe Gly Gly His Asn Ser>

 1300          1310          1320          1330          1340
GTT GTA GCT TTC TCA GCC TTC AAG CCA TGA TTA CTC GGT TCA AAT GCA
Val Val Ala Phe Ser Ala Phe Lys Pro
```

FIGURE 2

AATTTGTTGC TGAGACAGTG AGCTTCAACT TGCAGAGCAA TTTTTTTACAT GCCTTGTCGT

CGGAAGAGCG TAATACCGGG ATAGTTCCTT GATAGTTCAT TTAGGATGTT TTACTGCAAT

AATCGAAGAT TATTTCCATT CTAATCCAGT CTCCGNCGAG TTTGAGAATC TATCTGTTTG

TATTAGAAAG AACGAGGCAA GATTTTGTTT CATGTTTGTG TTTGTATTAC TTTCTTTTTG

CCCTTGTCAA TGGCATTTAA GATAAGCTTA TAAAAAAAAA AAAAAAAAAA AAAACTCGAG

GGGGGGCCCG GTACCCAATT CGCCCTATAG TGAGTCGTAT GACAATTCAC TGTCCGTCGG

FIGURE 2
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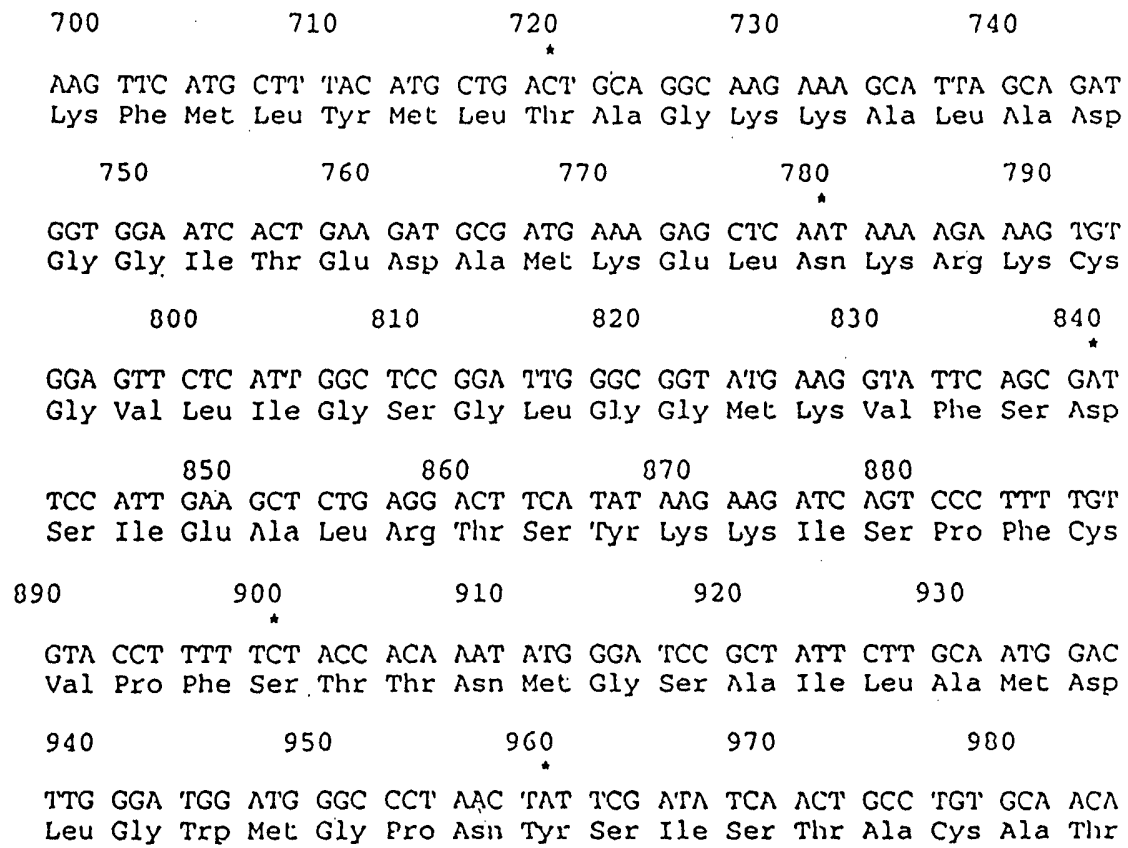
Sequence Range: 1 to 2046

```
          10         20         30         40         50         60
                                                                  *
ACTAAAGGGA ACAAAAGCTG GAGCTCCACC GCGGTGGCGG CCGCTCTAGA ACTAGTGGAT

          70         80         90        100        110        120
                                                                  *
CCCCCGGGCT GCAGGAATTC GGCACGAGTT TTCTTACTTG GTCGGCTCA GCTCAGGTGT

        130        140        150        160
TCCA ATG GCG ACC GCT TCT TGC ATG GTT GCG TCC CCT TTC TGT ACG TGG
     Met Ala Thr Ala Ser Cys Met Val Ala Ser Pro Phe Cys Thr Trp

170        180        190        200        210
           *
CTC GTA GCT GCA TGC ATG CCC ACT TCA TCC GAC AAC GAC CCA CGT TCC
Leu Val Ala Ala Cys Met Pro Thr Ser Ser Asp Asn Asp Pro Arg Ser

220        230        240        250        260
                      *
CTT TCC CAC AAG CGG CTC CGC CTC TCC CGT CGC CGG AGG ACT CTC TCC
Leu Ser His Lys Arg Leu Arg Leu Ser Arg Arg Arg Arg Thr Leu Ser

   270        280        290        300        310
                                    *
TCC CAT TGC TCC CTC CGC GGA TCC ACC TTC CAA TGC CTC GAT CCT TGC
Ser His Cys Ser Leu Arg Gly Ser Thr Phe Gln Cys Leu Asp Pro Cys

      320        330        340        350        360
                                                    *
AAC CAG CAA CGC TTC CTC GGG GAT AAC GGA TTC GCT TCC CTC TTC GGA
Asn Gln Gln Arg Phe Leu Gly Asp Asn Gly Phe Ala Ser Leu Phe Gly
```

FIGURE 3

```
          370           380           390           400
  TCC AAG CCT CTT CGT TCA AAT CGC GGC CAC CTG AGG CTC GGC CGC ACT
  Ser Lys Pro Leu Arg Ser Asn Arg Gly His Leu Arg Leu Gly Arg Thr

410           420           430           440           450
                *
  TCC CAT TCC GGG GAG GTC ATG GCT GTG GCT ATG CAA CCT GCA CAG GAA
  Ser His Ser Gly Glu Val Met Ala Val Ala Met Gln Pro Ala Gln Glu

  460           470           480           490           500
                              *
  GTC TCC ACA AAT AAG AAA CCT GCT ACC AAG CAA AGG CGA GTA GTT GTG
  Val Ser Thr Asn Lys Lys Pro Ala Thr Lys Gln Arg Arg Val Val Val

     510           520           530           540           550
                                               *
  ACA GGT ATG GGC GTG GTG ACT CCT CTA GGC CAT GAC CCC GAT GTT TAC
  Thr Gly Met Gly Val Val Thr Pro Leu Gly His Asp Pro Asp Val Tyr

        560           570           580           590           600
                                                                  *
  TAC AAC AAT CTC CTA GAC GGA ATA AGT GGC ATA AGT GAG ATA GAG AAC
  Tyr Asn Asn Leu Leu Asp Gly Ile Ser Gly Ile Ser Glu Ile Glu Asn

          610           620           630           640
  TTC GAC TGC TCT CAG TTT CCC ACG AGA ATT GCC GGA GAG ATC AAG TCT
  Phe Asp Cys Ser Gln Phe Pro Thr Arg Ile Ala Gly Glu Ile Lys Ser

650           660           670           680           690
                *
  TTT TCC ACA GAT GGC TGG GTG GCC CCA AAG TTC TCC GAG AGG ATG GAC
  Phe Ser Thr Asp Gly Trp Val Ala Pro Lys Phe Ser Glu Arg Met Asp
```

FIGURE 3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Lys Phe Met Leu Tyr Met Leu Thr Ala Gly Lys Lys Ala Leu Ala Asp
750 760 770 780 790
GGT GGA ATC ACT GAA GAT GCG ATG AAA GAG CTC AAT AAA AGA AAG TGT
Gly Gly Ile Thr Glu Asp Ala Met Lys Glu Leu Asn Lys Arg Lys Cys
800 810 820 830 840
GGA GTT CTC ATT GGC TCC GGA TTG GGC GGT ATG AAG GTA TTC AGC GAT
Gly Val Leu Ile Gly Ser Gly Leu Gly Gly Met Lys Val Phe Ser Asp
850 860 870 880
TCC ATT GAA GCT CTG AGG ACT TCA TAT AAG AAG ATC AGT CCC TTT TGT
Ser Ile Glu Ala Leu Arg Thr Ser Tyr Lys Lys Ile Ser Pro Phe Cys
890 900 910 920 930
GTA CCT TTT TCT ACC ACA AAT ATG GGA TCC GCT ATT CTT GCA ATG GAC
Val Pro Phe Ser Thr Thr Asn Met Gly Ser Ala Ile Leu Ala Met Asp
940 950 960 970 980
TTG GGA TGG ATG GGC CCT AAC TAT TCG ATA TCA ACT GCC TGT GCA ACA
Leu Gly Trp Met Gly Pro Asn Tyr Ser Ile Ser Thr Ala Cys Ala Thr

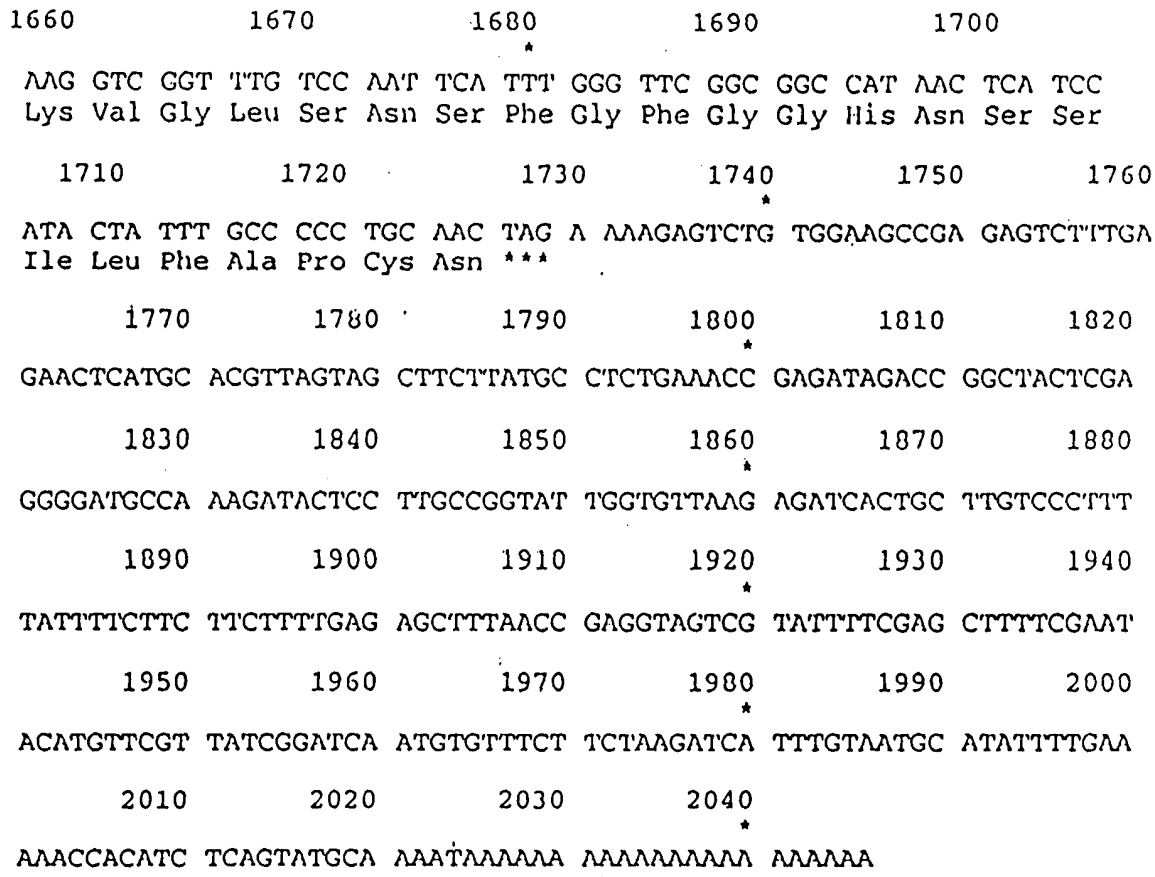
FIGURE 3

```
   990         1000          1010          1020          1030
                                            *
AGT AAC TTC TGT ATA CTG AAT GCT GCG AAC CAC ATA ATC AAA GGC GAA
Ser Asn Phe Cys Ile Leu Asn Ala Ala Asn His Ile Ile Lys Gly Glu

     1040          1050          1060          1070          1080
                                                               *
GCA GAC ATG ATG CTT TGT GGT GGC TCG GAT GCG GCC GTT TTA CCT GTT
Ala Asp Met Met Leu Cys Gly Gly Ser Asp Ala Ala Val Leu Pro Val

       1090          1100          1110          1120
GGT TTG GGA GGT TTC GTA GCA TGC CGA GCT TTG TCA CAG AGG AAT AAT
Gly Leu Gly Gly Phe Val Ala Cys Arg Ala Leu Ser Gln Arg Asn Asn

1130         1140          1150          1160          1170
                *
GAC CCT ACC AAA GCT TCG AGA CCA TGG GAC AGT AAT CGT GAT GGA TTT
Asp Pro Thr Lys Ala Ser Arg Pro Trp Asp Ser Asn Arg Asp Gly Phe

  1180          1190          1200          1210          1220
                                *
GTG ATG GGA GAA GGA GCT GGA GTT TTA CTT CTT GAG GAG TTA GAG CAT
Val Met Gly Glu Gly Ala Gly Val Leu Leu Leu Glu Glu Leu Glu His

    1230          1240          1250          1260          1270
                                                *
GCA AAG AAA AGA GGT GCA ACC ATT TAT GCG GAA TTT CTA GGT GGG AGT
Ala Lys Lys Arg Gly Ala Thr Ile Tyr Ala Glu Phe Leu Gly Gly Ser

     1280          1290          1300          1310          1320
                                                               *
TTC ACT TGC GAC GCC TAC CAC ATG ACC GAG CCT CAC CCT GAA GGA GCT
Phe Thr Cys Asp Ala Tyr His Met Thr Glu Pro His Pro Glu Gly Ala
```

FIGURE 3

```
        1330          1340          1350          1360
GGT GTG ATC CTC TGC ATA GAG AAG GCC TTG GCT CAG TCC GGA GTC TCG
Gly Val Ile Leu Cys Ile Glu Lys Ala Leu Ala Gln Ser Gly Val Ser

1370          1380          1390          1400          1410
                *
AGG GAA GAC GTA AAT TAC ATA AAT GCG CAT GCA ACT TCC ACT CCT GCT
Arg Glu Asp Val Asn Tyr Ile Asn Ala His Ala Thr Ser Thr Pro Ala

1420          1430          1440          1450          1460
                                  *
GGA GAT ATC AAG GAA TAC CAA GCT CTC GCC CAC TGT TTC GGC CAA AAC
Gly Asp Ile Lys Glu Tyr Gln Ala Leu Ala His Cys Phe Gly Gln Asn

1470          1480          1490          1500          1510
                                            *
AGT GAG CTG AGA GTG AAT TCC ACC AAA TCG ATG ATC GGT CAC CTT CTT
Ser Glu Leu Arg Val Asn Ser Thr Lys Ser Met Ile Gly His Leu Leu

1520          1530          1540          1550          1560
                                                          *
GGA GGA GCT GGT GGC GTA GAA GCA GTT GCA GTA GTT CAG GCA ATA AGG
Gly Gly Ala Gly Gly Val Glu Ala Val Ala Val Val Gln Ala Ile Arg

1570          1580          1590          1600
ACA GGA TGG ATC CAT CCA AAT ATT AAT TTG GAA GAC CCG GAC GAA GGC
Thr Gly Trp Ile His Pro Asn Ile Asn Leu Glu Asp Pro Asp Glu Gly

1610          1620          1630          1640          1650
                *
GTG GAT GCA AAA CTG CTC GTC GGC CCT AAG AAG GAG AAA CTG AAG GTC
Val Asp Ala Lys Leu Leu Val Gly Pro Lys Lys Glu Lys Leu Lys Val
```

FIGURE 3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Lys Val Gly Leu Ser Asn Ser Phe Gly Phe Gly Gly His Asn Ser Ser
1710 1720 1730 1740 1750 1760
ATA CTA TTT GCC CCC TGC AAC TAG A AAAGAGTCTG TGGAAGCCGA GAGTCTTTGA
Ile Leu Phe Ala Pro Cys Asn ***
1770 1780 1790 1800 1810 1820
GAACTCATGC ACGTTAGTAG CTTCTTATGC CTCTGAAACC GAGATAGACC GGCTACTCGA
1830 1840 1850 1860 1870 1880
GGGGATGCCA AAGATACTCC TTGCCGGTAT TGGTGTTAAG AGATCACTGC TTGTCCCTTT
1890 1900 1910 1920 1930 1940
TATTTTCTTC TTCTTTTGAG AGCTTTAACC GAGGTAGTCG TATTTTCGAG CTTTTCGAAT
1950 1960 1970 1980 1990 2000
ACATGTTCGT TATCGGATCA ATGTGTTTCT TCTAAGATCA TTTGTAATGC ATATTTTGAA
2010 2020 2030 2040
AAACCACATC TCAGTATGCA AAATAAAAAA AAAAAAAAAA AAAAAA

FIGURE 3
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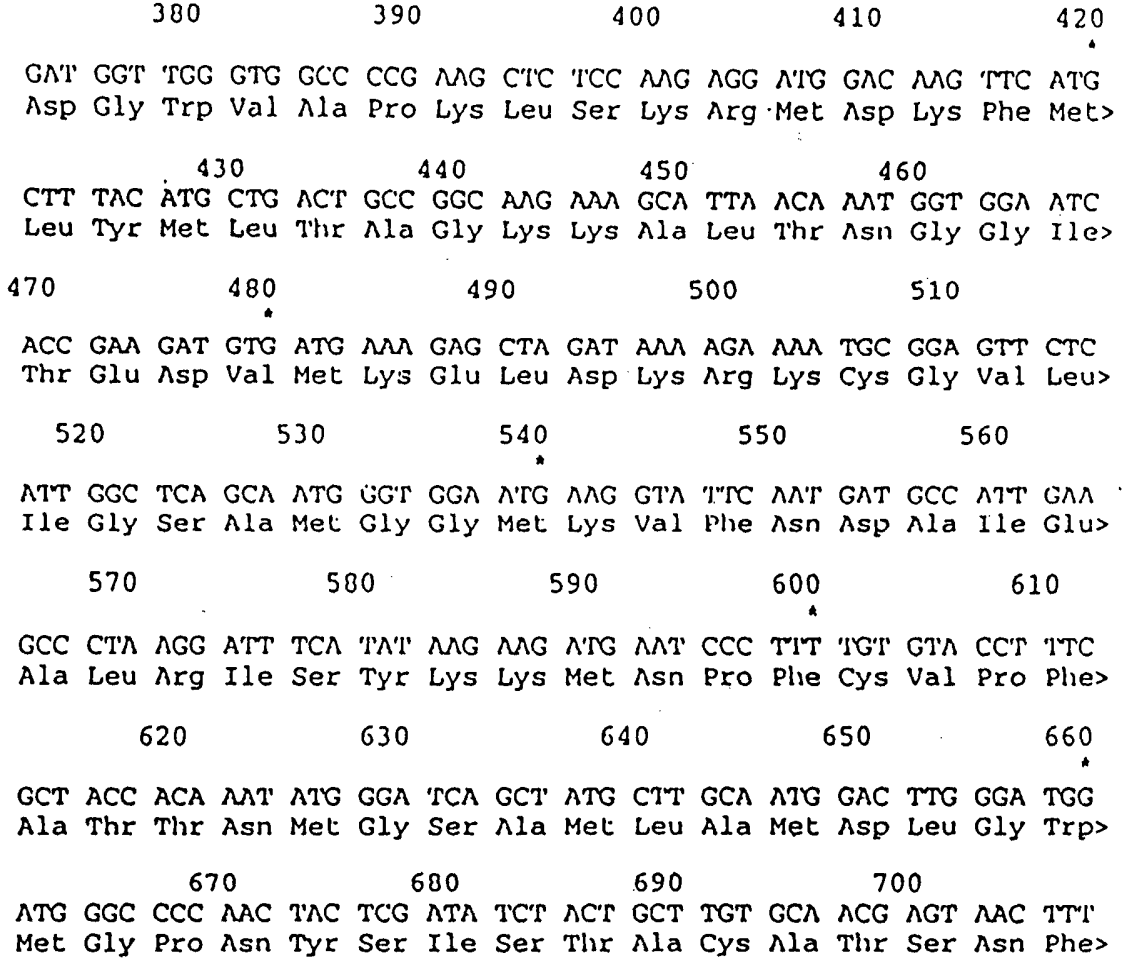
Sequence Range: 1 to 1921

```
          10         20         30         40         50         60
          *
CGGCACGAGG TCACCTCTTA CCTCGCCTGC TTCGAGCCCT GCCATGACTA CTACACCTCC

          70         80         90         100        110        120
                                                                  *
GCATCCTTGT TCGGATCCAG GCCCATCCGC ACCACCCGCA GGCACCGGAG GCTCAATCGA

         130        140        150        160        170        180
                                                                  *
GCTTCCCCTT CCGGGGAGGC AATGGCTGTG GCTCTGCAAC CTGCACAGGA AGTTACCACA

              190        200        210        220
AAG AAG AAG CCA AGT ATC AAA CAG CGG CGA GTA GTT GTG ACT GGA ATG
Lys Lys Lys Pro Ser Ile Lys Gln Arg Arg Val Val Val Thr Gly Met>

230           240        250        260        270
              *
GGT GTG GTG ACT CCT CTA GGC CAT GAC CCT GAT GTT TTC TAC AAT AAT
Gly Val Val Thr Pro Leu Gly His Asp Pro Asp Val Phe Tyr Asn Asn>

  280         290        300        310        320
                         *
CTG CTT GAT GGA ACG AGT GGC ATA AGT GAG ATA GAG ACC TTT GAT TGT
Leu Leu Asp Gly Thr Ser Gly Ile Ser Glu Ile Glu Thr Phe Asp Cys>

    330         340        350        360        370
                                      *
GCT CAA TTT CCT ACG AGA ATT GCT GGA GAG ATC AAG TCT TTC TCC ACA
Ala Gln Phe Pro Thr Arg Ile Ala Gly Glu Ile Lys Ser Phe Ser Thr>
```

FIGURE 4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Leu Tyr Met Leu Thr Ala Gly Lys Lys Ala Leu Thr Asn Gly Gly Ile>
470 480 490 500 510
ACC GAA GAT GTG ATG AAA GAG CTA GAT AAA AGA AAA TGC GGA GTT CTC
Thr Glu Asp Val Met Lys Glu Leu Asp Lys Arg Lys Cys Gly Val Leu>
520 530 540 550 560
ATT GGC TCA GCA ATG GGT GGA ATG AAG GTA TTC AAT GAT GCC ATT GAA
Ile Gly Ser Ala Met Gly Gly Met Lys Val Phe Asn Asp Ala Ile Glu>
570 580 590 600 610
GCC CTA AGG ATT TCA TAT AAG AAG ATG AAT CCC TTT TGT GTA CCT TTC
Ala Leu Arg Ile Ser Tyr Lys Lys Met Asn Pro Phe Cys Val Pro Phe>
620 630 640 650 660
GCT ACC ACA AAT ATG GGA TCA GCT ATG CTT GCA ATG GAC TTG GGA TGG
Ala Thr Thr Asn Met Gly Ser Ala Met Leu Ala Met Asp Leu Gly Trp>
670 680 690 700
ATG GGC CCC AAC TAC TCG ATA TCT ACT GCT TGT GCA ACG AGT AAC TTT
Met Gly Pro Asn Tyr Ser Ile Ser Thr Ala Cys Ala Thr Ser Asn Phe>

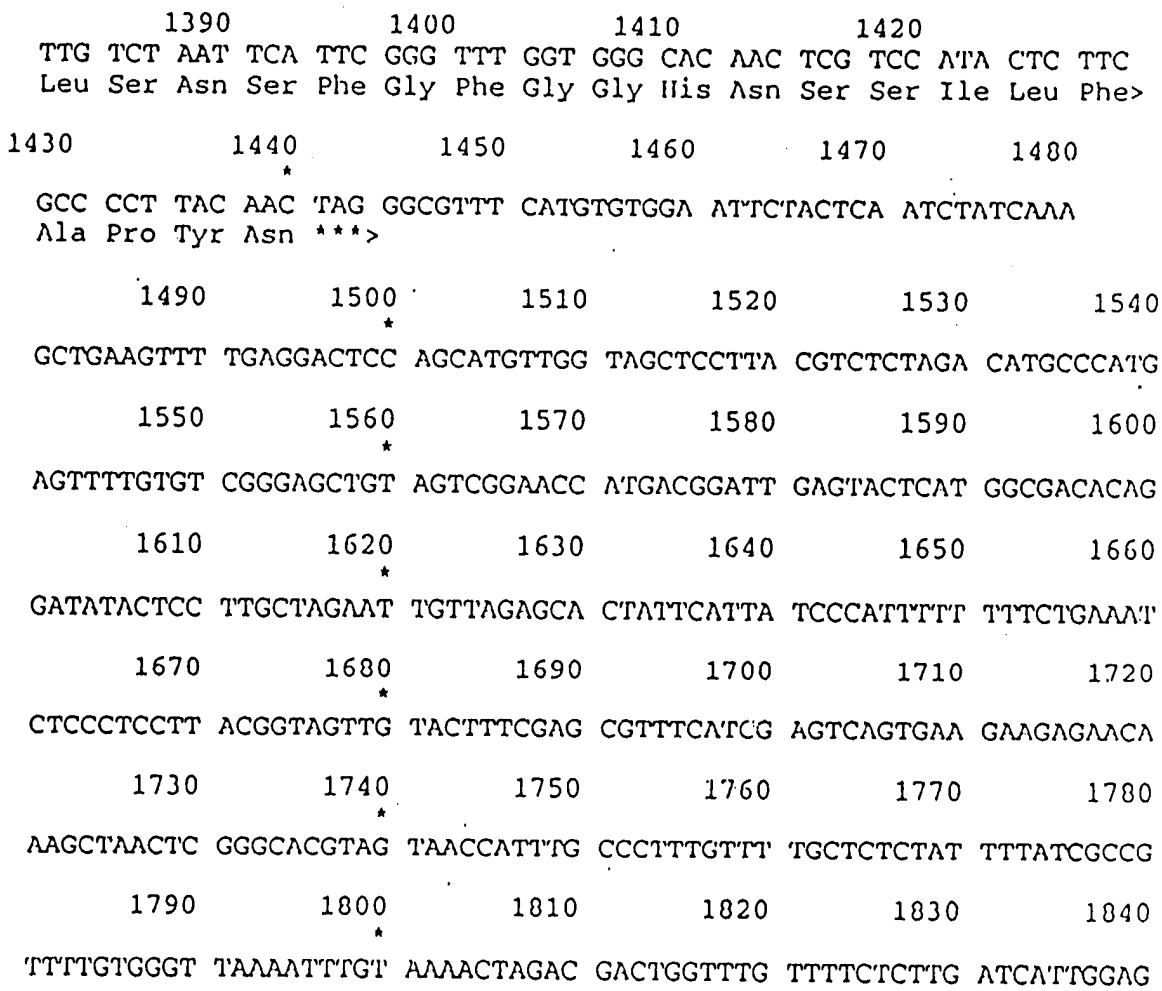
FIGURE 4

```
710          720          730          740          750
                *
TGT ATC CTG AAT GCT GCG AAC CAC ATA ATC AGA GGC GAA GCA GAT GTG
Cys Ile Leu Asn Ala Ala Asn His Ile Ile Arg Gly Glu Ala Asp Val>

  760          770          780          790          800
                            *
ATG CTT TGC GGG GGC TCA GAT GCG GTA ATC ATA CCT ATT GGT ATG GGA
Met Leu Cys Gly Gly Ser Asp Ala Val Ile Ile Pro Ile Gly Met Gly>

    810          820          830          840          850
                                           *
GGT TTT GTT GCA TGC CGA GCT TTG TCA CAG AGA AAT GCC GAC CCT ACT
Gly Phe Val Ala Cys Arg Ala Leu Ser Gln Arg Asn Ala Asp Pro Thr>

       860          870          880          890          900
                                                             *
AAA GCT TCA AGA CCA TGG GAC AGT AAT CGT GAT GGA TTT GTT ATG GGG
Lys Ala Ser Arg Pro Trp Asp Ser Asn Arg Asp Gly Phe Val Met Gly>

          910          920          930          940
GAA GGA GCT GGA GTG CTA CTA CTA GAG GAG TTA GAG CAT GCA AAG AAA
Glu Gly Ala Gly Val Leu Leu Leu Glu Glu Leu Glu His Ala Lys Lys>

950          960          970          980          990
                *
AGA GGT GCG ACT ATT TAC GCA GAA TTT CTA GGT GGA AGT TTC ACT TGC
Arg Gly Ala Thr Ile Tyr Ala Glu Phe Leu Gly Gly Ser Phe Thr Cys>

 1000         1010         1020         1030         1040
                           *
GAT GCC TAC CAC ATG ACC GAG CCT CAC CCT GAT GGA GCT GGA GTG ATT
Asp Ala Tyr His Met Thr Glu Pro His Pro Asp Gly Ala Gly Val Ile>
```

FIGURE 4

```
    1050          1060          1070          1080          1090
                                                *
CTC TGC ATA GAG AAG GCT TTG GCT CAG TCA GGA GTC TCT AGG GAA GAC
Leu Cys Ile Glu Lys Ala Leu Ala Gln Ser Gly Val Ser Arg Glu Asp>

      1100          1110          1120          1130          1140
                                                                *
GTA AAT TAC ATA AAT GCA CAT GCC ACA TCC ACT CCA GCT GGA GAT ATC
Val Asn Tyr Ile Asn Ala His Ala Thr Ser Thr Pro Ala Gly Asp Ile>

         1150          1160          1170          1180
AAA GAG TAC CAA GCT CTT ATC CAC TGT TTC GGC CAA AAC AAC GAG TTA
Lys Glu Tyr Gln Ala Leu Ile His Cys Phe Gly Gln Asn Asn Glu Leu>

1190          1200          1210          1220          1230
                  *
AAA GTG AAT TCT ACC AAA TCA ATG ATT GGT CAC CTT CTC GGA GCA GCC
Lys Val Asn Ser Thr Lys Ser Met Ile Gly His Leu Leu Gly Ala Ala>

 1240          1250          1260          1270          1280
                                  *
GGT GGT GTG GAA GCA GTT TCA GTA GTT CAG GCA ATA AGG ACT GGG TGG
Gly Gly Val Glu Ala Val Ser Val Val Gln Ala Ile Arg Thr Gly Trp>

   1290          1300          1310          1320          1330
                                                *
ATC CAT CCG AAT ATT AAT TTG GAA AAC CCA GAT GAA GGC GTG GAT ACC
Ile His Pro Asn Ile Asn Leu Glu Asn Pro Asp Glu Gly Val Asp Thr>

      1340          1350          1360          1370          1380
                                                                *
AAA TTG CTC GTG GGC CCT AAG AAG GAG AGA CTG AAC ATT AAG GTC GGT
Lys Leu Leu Val Gly Pro Lys Lys Glu Arg Leu Asn Ile Lys Val Gly>
```

FIGURE 4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Leu Ser Asn Ser Phe Gly Phe Gly Gly His Asn Ser Ser Ile Leu Phe>
1430 1440 1450 1460 1470 1480
GCC CCT TAC AAC TAG GGCGTTT CATGTGTGGA ATTCTACTCA ATCTATCAAA
Ala Pro Tyr Asn ***>
1490 1500 1510 1520 1530 1540
GCTGAAGTTT TGAGGACTCC AGCATGTTGG TAGCTCCTTA CGTCTCTAGA CATGCCCATG
1550 1560 1570 1580 1590 1600
AGTTTTGTGT CGGGAGCTGT AGTCGGAACC ATGACGGATT GAGTACTCAT GGCGACACAG
1610 1620 1630 1640 1650 1660
GATATACTCC TTGCTAGAAT TGTTAGAGCA CTATTCATTA TCCCATTTTT TTTCTGAAAT
1670 1680 1690 1700 1710 1720
CTCCCTCCTT ACGGTAGTTG TACTTTCGAG CGTTTCATCG AGTCAGTGAA GAAGAGAACA
1730 1740 1750 1760 1770 1780
AAGCTAACTC GGGCACGTAG TAACCATTTG CCCTTTGTTT TGCTCTCTAT TTTATCGCCG
1790 1800 1810 1820 1830 1840
TTTTGTGGGT TAAAATTTGT AAAACTAGAC GACTGGTTTG TTTTCTCTTG ATCATTGGAG

FIGURE 4

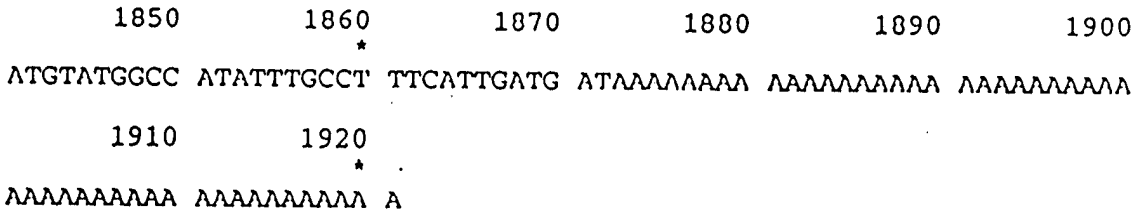

1850
1860
1870
1880
1890
1900
ATGTATGGCC ATATTTGCCT TTCATTGATG ATAAAAAAAA AAAAAAAAAA AAAAAAAAAA
1910
1920
AAAAAAAAAA AAAAAAAAAA A

FIGURE 4

```
CTGGTACGCC TGCAGGTACC GGTCCGGAAT TCCCGGGTCG ACCCACGCGT CCGTCTTCCC     60

ACTCCGATCG TTCTTCTTCC ACCGCATCTC TTCTCTTCTC TTGGCTTCTC CGCCATCCTC    120

CGCCGCC ATG CAT TCC CTC CAG TCA CCC TCC CTT CGG GCC TCC CCG CTC       169
        Met His Ser Leu Gln Ser Pro Ser Leu Arg Ala Ser Pro Leu
        1               5                   10

GAC CCC TTC CGC CCC AAA TCA TCC ACC GTC CGC CCC CTC CAC CGA GCA       217
Asp Pro Phe Arg Pro Lys Ser Ser Thr Val Arg Pro Leu His Arg Ala
15                  20                  25                  30

TCA ATT CCC AAC GTC CGG GCC GCT TCC CCC ACC GTC TCC GCT CCC AAG       265
Ser Ile Pro Asn Val Arg Ala Ala Ser Pro Thr Val Ser Ala Pro Lys
                    35                  40                  45

CGC GAG ACC GAC CCC AAG AAG CGC GTC GTG ATC ACC GGA ATG GGC CTT       313
Arg Glu Thr Asp Pro Lys Lys Arg Val Val Ile Thr Gly Met Gly Leu
            50                  55                  60

GTC TCC GTT TTC GGC TCC GAC GTC GAT GCG TAC TAC GAC AAG CTC CTG       361
Val Ser Val Phe Gly Ser Asp Val Asp Ala Tyr Tyr Asp Lys Leu Leu
        65                  70                  75

TCA GGC GAG AGC GGG ATC GGC CCA ATC GAC CGC TTC GAC GCC TCC AAG       409
Ser Gly Glu Ser Gly Ile Gly Pro Ile Asp Arg Phe Asp Ala Ser Lys
    80                  85                  90

TTC CCC ACC AGG TTC GGC GGC CAG ATT CGT GGC TTC AAC TCC ATG GGA       457
Phe Pro Thr Arg Phe Gly Gly Gln Ile Arg Gly Phe Asn Ser Met Gly
95                  100                 105                 110

TAC ATT GAC GGC AAA AAC GAC AGG CGG CTT GAT GAT TGC CTT CGC TAC       505
Tyr Ile Asp Gly Lys Asn Asp Arg Arg Leu Asp Asp Cys Leu Arg Tyr
                115                 120                 125
```

FIGURE 5

```
TGC ATT GTC GCC GGG AAG AAG TCT CTT GAG GAC GCC GAT CTC GGT GCC      553
Cys Ile Val Ala Gly Lys Lys Ser Leu Glu Asp Ala Asp Leu Gly Ala
            130                 135                 140

GAC CGC CTC TCC AAG ATC GAC AAG GAG AGA GCC GGA GTG CTG GTT GGG      601
Asp Arg Leu Ser Lys Ile Asp Lys Glu Arg Ala Gly Val Leu Val Gly
        145                 150                 155

ACA GGA ATG GGT GGT CTG ACT GTC TTC TCT GAC GGG GTT CAA TCT CTT      649
Thr Gly Met Gly Gly Leu Thr Val Phe Ser Asp Gly Val Gln Ser Leu
    160                 165                 170

ATC GAG AAG GGT CAC CGG AAA ATC ACC CCT TTC TTC ATC CCC TAT GCC      697
Ile Glu Lys Gly His Arg Lys Ile Thr Pro Phe Phe Ile Pro Tyr Ala
175                 180                 185                 190

ATT ACA AAC ATG GGG TCT GCC CTG CTC GCT ATT GAA CTC GGT CTG ATG      745
Ile Thr Asn Met Gly Ser Ala Leu Leu Ala Ile Glu Leu Gly Leu Met
                195                 200                 205

GGC CCA AAC TAT TCA ATT TCC ACT GCA TGT GCC ACT TCC AAC TAC TGC      793
Gly Pro Asn Tyr Ser Ile Ser Thr Ala Cys Ala Thr Ser Asn Tyr Cys
            210                 215                 220

TTC CAT GCT GCT GCT AAT CAT ATC CGC CGT GGT GAG GCT GAT CTT ATG      841
Phe His Ala Ala Ala Asn His Ile Arg Arg Gly Glu Ala Asp Leu Met
        225                 230                 235

ATT GCT GGA GGC ACT GAG GCC GCA ATC ATT CCA ATT GGG TTG GGA GGC      889
Ile Ala Gly Gly Thr Glu Ala Ala Ile Ile Pro Ile Gly Leu Gly Gly
    240                 245                 250
```

FIGURE 5
2/4

```
TTT GTG GCT TGC AGG GCT CTG TCT CAA AGG AAC GAT GAC CCT CAG ACT      937
Phe Val Ala Cys Arg Ala Leu Ser Gln Arg Asn Asp Asp Pro Gln Thr
255                 260                 265                 270

GCC TCT AGG CCC TGG GAT AAA GAC CGT GAT GGT TTT GTG ATG GGT GAA      985
Ala Ser Arg Pro Trp Asp Lys Asp Arg Asp Gly Phe Val Met Gly Glu
                275                 280                 285

GGT GCT GGA GTG TTG GTG CTG GAG AGC TTG GAA CAT GCA ATG AAA CGA     1033
Gly Ala Gly Val Leu Val Leu Glu Ser Leu Glu His Ala Met Lys Arg
            290                 295                 300

GGA GCA CCT ATT ATT GCA GAG TAT TTG GGA GGT GCA ATC AAC TGT GAT     1081
Gly Ala Pro Ile Ile Ala Glu Tyr Leu Gly Gly Ala Ile Asn Cys Asp
        305                 310                 315

GCT TAT CAC ATG ACT GAC CCA AGG GCT GAT GGT CTC GGT GTC TCC TCT     1129
Ala Tyr His Met Thr Asp Pro Arg Ala Asp Gly Leu Gly Val Ser Ser
    320                 325                 330

TGC ATT GAG AGT AGC CTT GAA GAT GCT GGC GTC TCA CCT GAA GAG GTC     1176
Cys Ile Glu Ser Ser Leu Glu Asp Ala Gly Val Ser Pro Glu Glu Val
335                 340                 345                 350

AAT TAC ATA AAT GCT CAT GCG ACT TCT ACT CTA GCT GGG GAT CTC GCC     1224
Asn Tyr Ile Asn Ala His Ala Thr Ser Thr Leu Ala Gly Asp Leu Ala
                355                 360                 365

GAG ATA AAT GCC ATC AAG AAG GTT TTC AAG AAC ACA AAG GAT ATC AAA     1272
Glu Ile Asn Ala Ile Lys Lys Val Phe Lys Asn Thr Lys Asp Ile Lys
            370                 375                 380
```

FIGURE 5

```
ATT AAT GCA ACT AAG TCA ATG ATC GGA CAC TGT CTT GGA GCC TCT GGA     1320
Ile Asn Ala Thr Lys Ser Met Ile Gly His Cys Leu Gly Ala Ser Gly
        385                 390                 395

GGT CTT GAA GCT ATA GCG ACT ATT AAG GGA ATA AAC ACC GGC TGG CTT     1368
Gly Leu Glu Ala Ile Ala Thr Ile Lys Gly Ile Asn Thr Gly Trp Leu
    400                 405                 410

CAT CCC AGC ATT AAT CAA TTC AAT CCT GAG CCA TCC GTG GAG TTC GAC     1416
His Pro Ser Ile Asn Gln Phe Asn Pro Glu Pro Ser Val Glu Phe Asp
415                 420                 425                 430

ACT GTT GCC AAC AAG AAG CAG CAA CAC GAA GTT AAT GTT GCG ATC TCG     1464
Thr Val Ala Asn Lys Lys Gln Gln His Glu Val Asn Val Ala Ile Ser
                435                 440                 445

AAT TCA TTT GGA TTC GGA GGC CAC AAC TCA GTC GTG GCT TTC TCG GCT     1512
Asn Ser Phe Gly Phe Gly Gly His Asn Ser Val Val Ala Phe Ser Ala
            450                 455                 460

TTC AAG CCA TGA TTACC CATTTCACAA GGCACTTGTC ATTGAGAGTA CGGTTGTTCG  1569
Phe Lys Pro
        465

TCAAACCCAT TTAGGATACT GTTCTATGTA AAAAAAAGTA AGGATTATCA CTTTCCCTTC  1629

TAATCCTGTC TCCAGTTTGA GAATGAAATT ATATTTATTT TAAAAAAAAA AAAAAAGGGC  1689

GGCCGCTCTA GAGGATCCAA GCT                                           1712
```

FIGURE 5

Sequence Range: 1 to 1802

```
          10         20         30         40         50         60
GGTCGACCCA CGCGTCCGGG CTTTCCGACC ACATTTCATT TCTTGCCTCG TTATCTCCGC

          70         80         90        100        110
CGCTCCTCCG CCGTCGTTCG CCGCCGCCGC C ATG CAA TCC CTC CAC TCC CCT TCC
                                   Met Gln Ser Leu His Ser Pro Ser

   120        130        140        150        160
CTC CGC CCC TCC CCT CTC GAG CCC TTC CGC CTC AAT TCC CCC TCC TCC
Leu Arg Pro Ser Pro Leu Glu Pro Phe Arg Leu Asn Ser Pro Ser Ser

       170        180        190        200        210
GCC GCC GCT CTC CGC CCC CTC CGT CGC GCC AGC CTC CCC GTC ATC CGT
Ala Ala Ala Leu Arg Pro Leu Arg Arg Ala Ser Leu Pro Val Ile Arg

         220        230        240        250
GCT GCC ACC GCC TCC GCC CCC AAG CGC GAG TCC GAC CCC AAG AAG CGG
Ala Ala Thr Ala Ser Ala Pro Lys Arg Glu Ser Asp Pro Lys Lys Arg

260        270        280        290        300
GTC GTC ATC ACC GGC ATG GGC CTC GTC TCC GTC TTC GGC TCC GAC GTC
Val Val Ile Thr Gly Met Gly Leu Val Ser Val Phe Gly Ser Asp Val

310        320        330        340        350
GAC GCC TAC TAC GAC AAG CTG CTC TCC GGC GAG AGC GGC ATC AGC CTA
Asp Ala Tyr Tyr Asp Lys Leu Leu Ser Gly Glu Ser Gly Ile Ser Leu
```

FIGURE 6

```
   360          370          380          390          400
    *
ATC GAC CGC TTC GAC GCT TCC AAA TTC CCC ACC AGG TTC GCC GGC CAG
Ile Asp Arg Phe Asp Ala Ser Lys Phe Pro Thr Arg Phe Ala Gly Gln

      410          420          430          440          450
                    *
ATC CGT GGC TTC AAC GCG ACG GGC TAC ATC GAC GGC AAG AAC GAC CGG
Ile Arg Gly Phe Asn Ala Thr Gly Tyr Ile Asp Gly Lys Asn Asp Arg

        460          470          480          490
                                   *
CGG CTC GAC GAT TGC CTC CGC TAC TGC ATT GTC GCC GGC AAG AAG GCT
Arg Leu Asp Asp Cys Leu Arg Tyr Cys Ile Val Ala Gly Lys Lys Ala

500          510          520          530          540
                                                     *
CTC GAA GAC GCC GAT CTC GCC GGC CAA TCC CTC TCC AAG ATT GAT AAG
Leu Glu Asp Ala Asp Leu Ala Gly Gln Ser Leu Ser Lys Ile Asp Lys

550          560          570          580          590
GAG AGG GCC GGA GTG CTA GTT GGA ACC GGT ATG GGT GGC CTA ACT GTC
Glu Arg Ala Gly Val Leu Val Gly Thr Gly Met Gly Gly Leu Thr Val

   600          610          620          630          640
    *
TTC TCT GAC GGG GTT CAG AAT CTC ATC GAG AAA GGT CAC CGG AAG ATC
Phe Ser Asp Gly Val Gln Asn Leu Ile Glu Lys Gly His Arg Lys Ile

      650          660          670          680          690
                    *
TCC CCG TTT TTC ATT CCA TAT GCC ATT ACA AAC ATG GGG TCT GCG CTG
Ser Pro Phe Phe Ile Pro Tyr Ala Ile Thr Asn Met Gly Ser Ala Leu
```

FIGURE 6

```
          700           710           720           730
                                      *
CTT GCC ATC GAT TTG GGT CTG ATG GGC CCA AAC TAT TCG ATT TCA ACT
Leu Ala Ile Asp Leu Gly Leu Met Gly Pro Asn Tyr Ser Ile Ser Thr

740           750           760           770           780
                                                          *
GCA TGT GCT ACT TCC AAC TAC TGC TTT TAT GCT GCC GCC AAT CAT ATC
Ala Cys Ala Thr Ser Asn Tyr Cys Phe Tyr Ala Ala Ala Asn His Ile

790           800           810           820           830
CGC CGA GGT GAG GCT GAC CTG ATG ATT GCT GGA GGA ACT GAG GCT GCG
Arg Arg Gly Glu Ala Asp Leu Met Ile Ala Gly Gly Thr Glu Ala Ala

   840           850           860           870           880
    *
GTC ATT CCA ATT GGT TTA GGA GGA TTC GTT GCC TGC AGG GCT TTA TCT
Val Ile Pro Ile Gly Leu Gly Gly Phe Val Ala Cys Arg Ala Leu Ser

      890           900           910           920           930
                    *
CAA AGG AAT GAT GAT CCT CAG ACT GCC TCA AGG CCG TGG GAT AAG GAC
Gln Arg Asn Asp Asp Pro Gln Thr Ala Ser Arg Pro Trp Asp Lys Asp

      940           950           960           970
                                    *
CGT GAT GGC TTT GTG ATG GGT GAA GGG GCT GGA GTA TTG GTT ATG GAG
Arg Asp Gly Phe Val Met Gly Glu Gly Ala Gly Val Leu Val Met Glu

980           990           1000          1010          1020
                                                          *
AGC TTG GAG CAT GCA ATG AAA CGG GGA GCG CCG ATT ATT GCA GAA TAT
Ser Leu Glu His Ala Met Lys Arg Gly Ala Pro Ile Ile Ala Glu Tyr
```

FIGURE 6

```
1030          1040          1050          1060          1070
TTG GGA GGT GCA GTC AAC TGT GAT GCT TAT CAT ATG ACT GAT CCA AGG
Leu Gly Gly Ala Val Asn Cys Asp Ala Tyr His Met Thr Asp Pro Arg

  1080          1090          1100          1110          1120
  *
GCT GAT GGG CTT GGT GTC TCC TCG TGC ATT GAG AGC AGT CTC GAA GAT
Ala Asp Gly Leu Gly Val Ser Ser Cys Ile Glu Ser Ser Leu Glu Asp

      1130          1140          1150          1160          1170
                    *
GCC GGG GTC TCA CCT GAA GAG GTC AAT TAC ATA AAT GCT CAT GCG ACT
Ala Gly Val Ser Pro Glu Glu Val Asn Tyr Ile Asn Ala His Ala Thr

        1180          1190          1200          1210
                                    *
TCT ACT CTT GCT GGG GAT CTT GCC GAG ATA AAT GCC ATT AAG AAA GTT
Ser Thr Leu Ala Gly Asp Leu Ala Glu Ile Asn Ala Ile Lys Lys Val

1220          1230          1240          1250          1260
                                                        *
TTC AAG AAC ACC AAG GAA ATC AAA ATC AAT GCA ACT AAG TCA ATG ATC
Phe Lys Asn Thr Lys Glu Ile Lys Ile Asn Ala Thr Lys Ser Met Ile

1270          1280          1290          1300          1310
GGA CAC TGT CTT GGA GCA TCA GGA GGT CTT GAA GCC ATC GCA ACC ATT
Gly His Cys Leu Gly Ala Ser Gly Gly Leu Glu Ala Ile Ala Thr Ile

  1320          1330          1340          1350          1360
  *
AAG GGA ATA ACC ACC GGC TGG CTT CAT CCC AGC ATT AAT CAA TTT AAT
Lys Gly Ile Thr Thr Gly Trp Leu His Pro Ser Ile Asn Gln Phe Asn
```

FIGURE 6

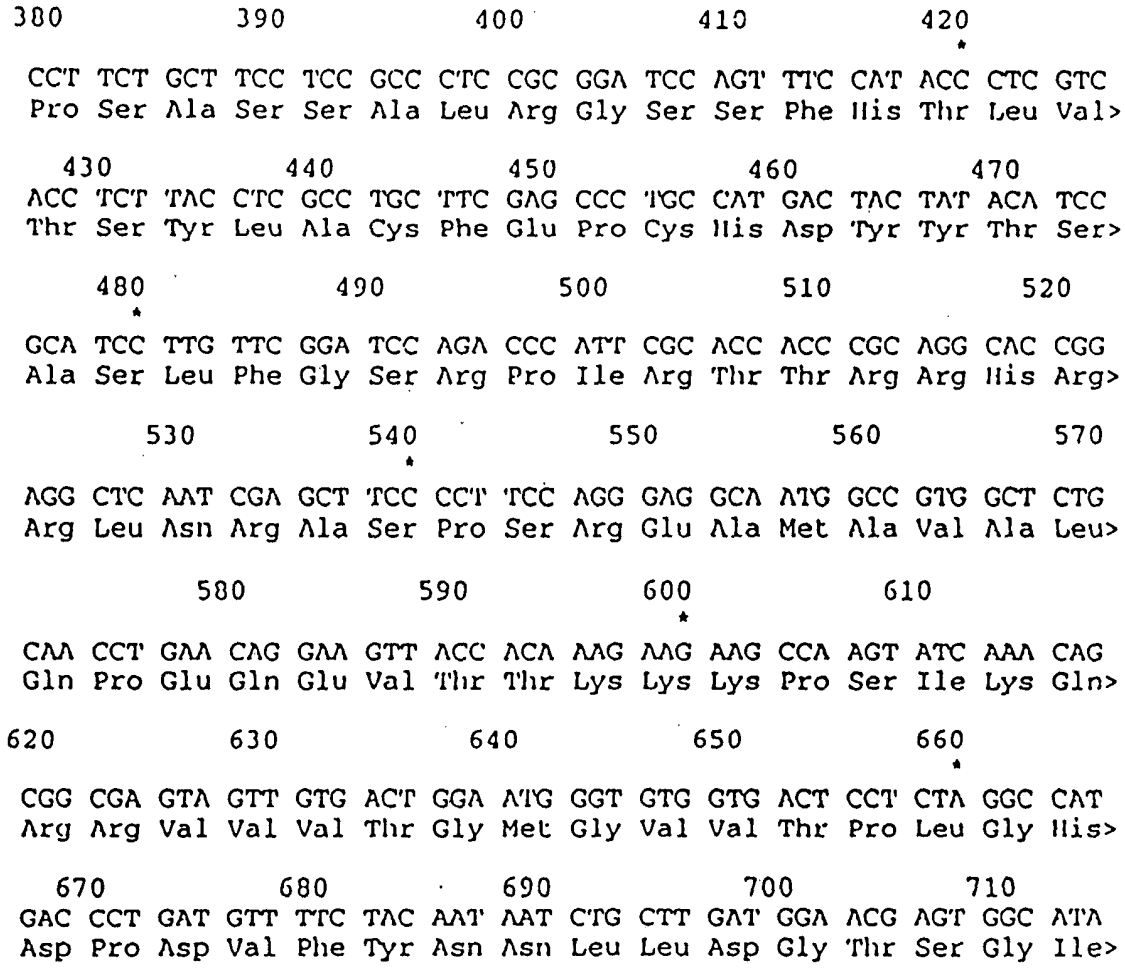
```
      1370         1380         1390         1400         1410
                    *
CCC GAG CCA TCG GTG GAC TTC AAC ACT GTT GCC AAC AAA AAG CAG CAA
Pro Glu Pro Ser Val Asp Phe Asn Thr Val Ala Asn Lys Lys Gln Gln

       1420         1430         1440         1450
                                   *
CAT GAA GTG AAC GTC GCT ATC TCG AAT TCT TTT GGA TTT GGA GGG CAC
His Glu Val Asn Val Ala Ile Ser Asn Ser Phe Gly Phe Gly Gly His

1460         1470         1480         1490         1500         1510
                                                      *
AAC TCG GTT GTG GCA TTC TCA GCT TTC AAG CCA TGA ATTCT ACTTGGTTCA
Asn Ser Val Val Ala Phe Ser Ala Phe Lys Pro ***

      1520         1530         1540         1550         1560         1570
                                                            *
AAATGCACAC CAGTTGCTGA GATAGGGCTT CAACTTGCAG AGCAATTTTT TAAATGCCTT

      1580         1590         1600         1610         1620         1630
                                                            *
GTCGGAAGAG CGTAATACCG GAATAGGTCG GTCCTTTGAT AGTTCCTCGA AGCCATTTAG

      1640         1650         1660         1670         1680         1690
                                                            *
GATGATGTTT TACTGTAATA ATCGAAGATG ATTCCCATTT TAAATCTAGT CTCTGATTTA

      1700         1710         1720         1730         1740         1750
                                                            *
TGTATTAGAA AGACCAATGA AAGATTTTGT GTCATGTTTG TGTTGTCAAT GTTATTTAAG

      1760         1770         1780         1790         1800
                                                            *
ATAAAGCAAA AAAAAAAAAA AAGGGCGGCC GCTCTAGAGG ATCCAGCTTA CT
```

FIGURE 6

Sequence Range: 1 to 2369

```
          10         20         30         40         50         60
GTACGCCTGC AGGTACCGGT CCGGAATTCC CGGGTCGACC CACGCGTCCG CATAAAAGAG

          70         80         90        100        110        120
AGAGAGAGGG ATCCATCGAA TGCGGCCACC CTCCTTTCAT CTTCGATTCA TTACCATACC

         130        140        150        160        170        180
ATTCCGCTGA TCCATTTTCC GCCTTTTCCG GGTCTTTCAT CCCAAAGGGT ATCCTTTTCT

         190        200        210        220        230
ATCCTATCTT CTCAAAGGGT CAGTCAGTTC CCTCCA ATG CCT GCC GCC TCT TCC
                                        Met Pro Ala Ala Ser Ser>

     240        250        260        270        280
CTG CTC GCT TCC CCT CTC TGT ACG TGG CTC CTT GCC GCC TGC ATG TCT
Leu Leu Ala Ser Pro Leu Cys Thr Trp Leu Leu Ala Ala Cys Met Ser>

        290        300        310        320        330
ACC TCC TTC CAC CCC TCC GAC CCT CTT CCG CCT TCC ATC TCC TCT CCT
Thr Ser Phe His Pro Ser Asp Pro Leu Pro Pro Ser Ile Ser Ser Pro>

           340        350        360        370
CGC CGA CGC CTC TCC CGC CGC CGG ATT CTC TCC CAA TGC GCC CCA CTA
Arg Arg Arg Leu Ser Arg Arg Arg Ile Leu Ser Gln Cys Ala Pro Leu>
```

FIGURE 7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Pro Ser Ala Ser Ser Ala Leu Arg Gly Ser Ser Phe His Thr Leu Val>
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ACC TCT TAC CTC GCC TGC TTC GAG CCC TGC CAT GAC TAC TAT ACA TCC
Thr Ser Tyr Leu Ala Cys Phe Glu Pro Cys His Asp Tyr Tyr Thr Ser>
480 490 500 510 520
GCA TCC TTG TTC GGA TCC AGA CCC ATT CGC ACC ACC CGC AGG CAC CGG
Ala Ser Leu Phe Gly Ser Arg Pro Ile Arg Thr Thr Arg Arg His Arg>
530 540 550 560 570
AGG CTC AAT CGA GCT TCC CCT TCC AGG GAG GCA ATG GCC GTG GCT CTG
Arg Leu Asn Arg Ala Ser Pro Ser Arg Glu Ala Met Ala Val Ala Leu>
580 590 600 610
CAA CCT GAA CAG GAA GTT ACC ACA AAG AAG AAG CCA AGT ATC AAA CAG
Gln Pro Glu Gln Glu Val Thr Thr Lys Lys Lys Pro Ser Ile Lys Gln>
620 630 640 650 660
CGG CGA GTA GTT GTG ACT GGA ATG GGT GTG GTG ACT CCT CTA GGC CAT
Arg Arg Val Val Val Thr Gly Met Gly Val Val Thr Pro Leu Gly His>
670 680 690 700 710
GAC CCT GAT GTT TTC TAC AAT AAT CTG CTT GAT GGA ACG AGT GGC ATA
Asp Pro Asp Val Phe Tyr Asn Asn Leu Leu Asp Gly Thr Ser Gly Ile>

FIGURE 7

```
     720           730           740           750           760
      *
AGC GAG ATA GAG ACC TTT GAT TGT GCT CAA TTT CCT ACG AGA ATT GCT
Ser Glu Ile Glu Thr Phe Asp Cys Ala Gln Phe Pro Thr Arg Ile Ala>

        770           780           790           800           810
                      *
GGA GAG ATC AAG TCT TTC TCC ACA GAT GGT TGG GTG GCC CCG AAG CTC
Gly Glu Ile Lys Ser Phe Ser Thr Asp Gly Trp Val Ala Pro Lys Leu>

           820           830           840           850
                                       *
TCT AAG AGG ATG GAC AAG TTC ATG CTA TAC ATG CTG ACC GCT GGC AAG
Ser Lys Arg Met Asp Lys Phe Met Leu Tyr Met Leu Thr Ala Gly Lys>

860           870           880           890           900
                                                          *
AAA GCA TTA ACA GAT GGT GGA ATC ACC GAA GAT GTG ATG AAA GAG CTA
Lys Ala Leu Thr Asp Gly Gly Ile Thr Glu Asp Val Met Lys Glu Leu>

  910           920           930           940           950
GAT AAA AGA AAA TGC GGA GTT CTC ATT GGC TCA GCA ATG GGT GGA ATG
Asp Lys Arg Lys Cys Gly Val Leu Ile Gly Ser Ala Met Gly Gly Met>

     960           970           980           990          1000
      *
AAG GTA TTC AAT GAT GCC ATT GAA GCC CTA AGG ATT TCA TAT AAG AAG
Lys Val Phe Asn Asp Ala Ile Glu Ala Leu Arg Ile Ser Tyr Lys Lys>

       1010          1020          1030          1040          1050
                     *
ATG AAT CCC TTT TGT GTA CCT TTC GCT ACC ACA AAT ATG GGA TCA GCT
Met Asn Pro Phe Cys Val Pro Phe Ala Thr Thr Asn Met Gly Ser Ala>
```

FIGURE 7

```
          1060         1070         1080         1090
ATG CTT GCA ATG GAC TTG GGA TGG ATG GGG CCC AAC TAC TCG ATA TCT
Met Leu Ala Met Asp Leu Gly Trp Met Gly Pro Asn Tyr Ser Ile Ser>

1100         1110         1120         1130         1140
ACT GCT TGT GCA ACG AGT AAC TTT TGT ATA ATG AAT GCT GCG AAC CAT
Thr Ala Cys Ala Thr Ser Asn Phe Cys Ile Met Asn Ala Ala Asn His>

 1150         1160         1170         1180         1190
ATA ATC AGA GGC GAA GCA GAT GTG ATG CTT TGC GGG GGC TCA GAT GCG
Ile Ile Arg Gly Glu Ala Asp Val Met Leu Cys Gly Gly Ser Asp Ala>

   1200         1210         1220         1230         1240
GTA ATC ATA CCT ATT GGT ATG GGA GGT TTT GTT GCA TGC CGA GCT TTG
Val Ile Ile Pro Ile Gly Met Gly Gly Phe Val Ala Cys Arg Ala Leu>

      1250         1260         1270         1280         1290
TCC CAG AGA AAT TCC GAC CCT ACT AAA GCT TCA AGA CCA TGG GAC AGT
Ser Gln Arg Asn Ser Asp Pro Thr Lys Ala Ser Arg Pro Trp Asp Ser>

          1300         1310         1320         1330
AAT CGT GAT GGA TTT GTT ATG GGG GAA GGA GCT GGA GTG CTA CTA CTA
Asn Arg Asp Gly Phe Val Met Gly Glu Gly Ala Gly Val Leu Leu Leu>

1340         1350         1360         1370         1380
GAG GAG TTG GAG CAT GCA AAG AAA AGA GGT GCG ACT ATT TAC GCA GAA
Glu Glu Leu Glu His Ala Lys Lys Arg Gly Ala Thr Ile Tyr Ala Glu>
```

FIGURE 7

```
 1390          1400          1410          1420          1430
TTT CTA GGT GGG AGT TTC ACT TGC GAT GCC TAC CAC ATG ACC GAG CCT
Phe Leu Gly Gly Ser Phe Thr Cys Asp Ala Tyr His Met Thr Glu Pro>

   1440          1450          1460          1470          1480
    *
CAC CCT GAT GGA GCT GGA GTG ATT CTC TGC ATA GAG AAG GCT TTG GCT
His Pro Asp Gly Ala Gly Val Ile Leu Cys Ile Glu Lys Ala Leu Ala>

      1490          1500          1510          1520          1530
                     *
CAG TCA GGA GTC TCT AGG GAA GAC GTA AAT TAC ATA AAT GCC CAT GCC
Gln Ser Gly Val Ser Arg Glu Asp Val Asn Tyr Ile Asn Ala His Ala>

          1540          1550          1560          1570
                                       *
ACA TCC ACT CCG GCT GGA GAT ATC AAA GAG TAC CAA GCT CTT ATC CAC
Thr Ser Thr Pro Ala Gly Asp Ile Lys Glu Tyr Gln Ala Leu Ile His>

1580          1590          1600          1610          1620
                                                          *
TGT TTC GGC CAA AAC AGA GAG TTA AAA GTT AAT TCA ACC AAA TCA ATG
Cys Phe Gly Gln Asn Arg Glu Leu Lys Val Asn Ser Thr Lys Ser Met>

 1630          1640          1650          1660          1670
ATT GGT CAC CTT CTC GGA GCA GCC GGT GGT GTG GAA GCA GTT TCA GTA
Ile Gly His Leu Leu Gly Ala Ala Gly Gly Val Glu Ala Val Ser Val>

   1680          1690          1700          1710          1720
    *
GTT CAG GCA ATA AGG ACT GGG TGG ATC CAT CCG AAT ATT AAT TTG GAA
Val Gln Ala Ile Arg Thr Gly Trp Ile His Pro Asn Ile Asn Leu Glu>
```

FIGURE 7

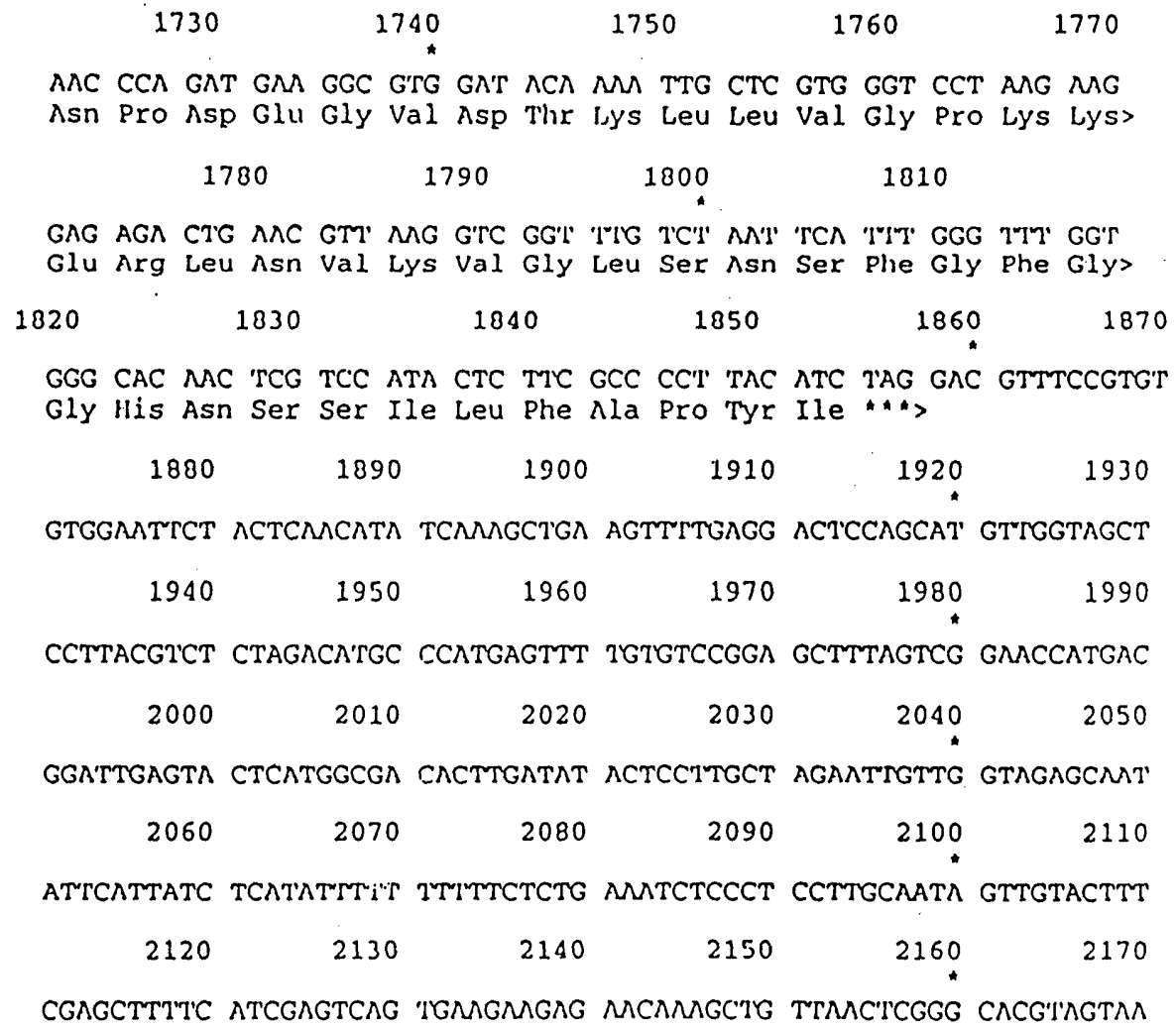

1730 1740 1750 1760 1770
AAC CCA GAT GAA GGC GTG GAT ACA AAA TTG CTC GTG GGT CCT AAG AAG
Asn Pro Asp Glu Gly Val Asp Thr Lys Leu Leu Val Gly Pro Lys Lys>
1780 1790 1800 1810
GAG AGA CTG AAC GTT AAG GTC GGT TTG TCT AAT TCA TTT GGG TTT GGT
Glu Arg Leu Asn Val Lys Val Gly Leu Ser Asn Ser Phe Gly Phe Gly>
1820 1830 1840 1850 1860 1870
GGG CAC AAC TCG TCC ATA CTC TTC GCC CCT TAC ATC TAG GAC GTTTCCGTGT
Gly His Asn Ser Ser Ile Leu Phe Ala Pro Tyr Ile ***>
1880 1890 1900 1910 1920 1930
GTGGAATTCT ACTCAACATA TCAAAGCTGA AGTTTTGAGG ACTCCAGCAT GTTGGTAGCT
1940 1950 1960 1970 1980 1990
CCTTACGTCT CTAGACATGC CCATGAGTTT TGTGTCCGGA GCTTTAGTCG GAACCATGAC
2000 2010 2020 2030 2040 2050
GGATTGAGTA CTCATGGCGA CACTTGATAT ACTCCTTGCT AGAATTGTTG GTAGAGCAAT
2060 2070 2080 2090 2100 2110
ATTCATTATC TCATATTTTT TTTTTCTCTG AAATCTCCCT CCTTGCAATA GTTGTACTTT
2120 2130 2140 2150 2160 2170
CGAGCTTTTC ATCGAGTCAG TGAAGAAGAG AACAAAGCTG TTAACTCGGG CACGTAGTAA

FIGURE 7

```
      2180        2190        2200        2210        2220        2230
CCATTTGCCC TTTGTTTTGC TCTCTATTTC ATCACCGTTT TGTGGTTTTA AAATTTGTAA
      2240        2250        2260        2270        2280        2290
AACTAGAAGA CTGGTTTAGA TTGGTTTGTT TTCTCATTGA TAATTGGGGR ATGTATGTTT
      2300        2310        2320        2330        2340        2350
TGGAAATAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA
      2360
AGGGCGGCCG CTCTAGAGG
```

FIGURE 7

Sequence Range: 1 to 2374

```
        10         20         30         40         50         60
-A-CNTGGTC CGGAATTCCC GGGTCGACCC ACGCGTCCGC GACGCCAACC CACACCAAAC
        70         80         90        100        110        120
TTCCTCAGCT TCTCTTCTCA AGACGGACGC CATTGGCAGC AGACAGACAG ACAGACAGAC
       130        140        150        160        170        180
CCATAAAAGA GAGAGAGAGG GATCCATCGA ATGCGGCCAC CCTCCTTTCA TCTTCGATTC
       190        200        210        220        230        240
ATTACCATAC CATTCCGCTG ATCCATTTTC CGCCTTTTCC GGGTCTTTCA TCCCAAAGGG
       250        260        270        280        290        300
TATCCTTTTC TATCCTATCT TCTCAAAGGG TCAGTCAGTT CCCTCCAATG CCTGCCGCCT
       310        320        330        340        350        360
CTTCCCTGCT CGCTTCCCCT CTCTGTACGT GGCTCCTTGC CGCCTGCATG TCTACCTCCT
       370        380        390        400        410        420
TCCACCCCTC CGACCCTCTT CCGCCTTCCA TCTCCTCTCC TCGCCGACGC CTCTCCCGCC
       430        440        450        460        470        480
GCCGGATTCT CTCCCAATGC GCCCCACTAC CTTCTGCTTC CTCCGCCCTC CGCGGATCCA
```

FIGURE 8
1/5

```
      490        500        510        520        530        540
       .          .          .          .          .          .
GTTTCCATAC CCTCGTCACC TCTTACCTCG CCTGCTTCGA GCCCTGCCAT GACTACTATA

      550        560        570        580        590        600
       .          .          .          .          .          .
CATCCGCATC CTTGTTCGGA TCCAGACCCA TTCGCACCAC CCGCAGGCAC CGGAGGCTCA

      610        620        630        640        650        660
       .          .          .          .          .          .
ATCGAGCTTC CCCTTCCAGG GGAGGCAATG GCCGTGGCTC TGCAACCTGA ACAGGAAGTT

      670        680        690        700        710        720
       .          .          .          .          .          .
ACCACAAAGA AGAAGCCAAG TATCAAACAG CGGCGAGTAG TTGTGACTGG AATGGGTGTG

      730        740        750        760        770        780
       .          .          .          .          .          .
GTGACTCCTC TAGGCCATGA ACCTGATGTT TTTCTACAAT AATCTGCTTG ATGGAACGAG

      790        800        810        820        830        840
       .          .          .          .          .          .
TGGCATAAGC GAGATAGAGA CCTTTGATTG TGCTCAATTT CCTACGAGAA TTGCTGGAGA

      850        860        870        880        890        900
       .          .          .          .          .          .
GATCAAGTCT TTCTCCACAG ATGGTTGGGT GGCCCCGAAG CTCTCTAAGA GGATGGACAA

      910        920        930        940        950        960
       .          .          .          .          .          .
GTTCATGCTA TACATGCTGA CTGCTGGCAA GAAGCATTTA ACAGATGGTG GAATCACCGA

      970        980        990        1000       1010       1020
       .          .          .          .          .          .
AGATGTGATG AAAGAGCTAG ATAAAAGAAA ATGCGGAGTT CTCATTGGCT CAGCAATGGG
```

FIGURE 8
2/5

```
      1030        1040        1050        1060        1070        1080
TGGAATGAAG GTATTCAATG ATGCCATTGA AGCCCTAAGG ATTTCATATA AGAAGATGAA
      1090        1100        1110        1120        1130        1140
TCCCTTTTGT GTACCTTTCG CTACCACAAA TATGGGATCA GCTATGCTTG CAATGGACTT
      1150        1160        1170        1180        1190        1200
GGGATGGATG GGGCCCAACT ACTCGATATC TACTGCTTGT GCAACGAGTA ACTTTTGTAT
      1210        1220        1230        1240        1250        1260
AATGAATGCT GCGAACCATA TAATCAGAGG CGAAGCAGAT GTGATGCTTT GCGGGGGCTC
      1270        1280        1290        1300        1310        1320
AGATGCGGTA ATCATACCTA TTGGTATGGG AGGTTTTTGT GCATGCCGAG CTTTGTCCCA
      1330        1340        1350        1360        1370        1380
GAGAAATTCC GACCCTACTA AAGCTTCAAG ACCATGGGAC AGTAATCGTG ATGGATTTGT
      1390        1400        1410        1420        1430        1440
TATGGGGGAA GGAGCTGGAG TGCTACTACT AGAGGAGTTG GAGCATGCAA AGAAAAGAGG
      1450        1460        1470        1480        1490        1500
TGCGACTATT TACGCAGAAT TTCTAGGTGG GAGTTTCACT TGCGATGCCT ACCACATGAC
```

FIGURE 8
3/5

1510 1520 1530 1540 1550 1560

CGAGCCTCAC CCTGATGGAG CTGGAGTGAT TCTCTGCATA GAGAAGGCTT TGGCTCAGTC

1570 1580 1590 1600 1610 1620

AGGAGTCTCT AGGGAAGACG TAAATTTACAT AAATGCCCAT GCCACATCCA CTCCGGCTGG

1630 1640 1650 1660 1670 1680

AGATATCAAA GAGTACCAAG CTCTTATCCA CTGTTTCGGC CAAAACAGAG AGTTAAAAGT

1690 1700 1710 1720 1730 1740

TAATTCAACC AAATCAATGA TTGGTCACCT TCTCGGAGCA GCCGGTGGTG TGGAAGCAGT

1750 1760 1770 1780 1790 1800

TTCAGTAGTT CAGGCAATAA GGACTGGGTG GATCCATCCG AATATTAATT TGGAAAACCC

1810 1820 1830 1840 1850 1860

AGATGAAGGC GTGGATACAA AATTGCTCGT GGGTCCTAAG AAGGAGAGAC TGAACGTTAA

1870 1880 1890 1900 1910 1920

GGTCGGTTTG TCTAATTCAT TTGGGTTTGG TGGGCACAAC TCGTCCATAC TCTTCGCCCC

1930 1940 1950 1960 1970 1980

TTACATCTAG GACGTTTCGT GTGTGGAATT CTACTCAACA TATCAAAGCT GAAGTTTTGA

1990 2000 2010 2020 2030 2040

GGACTCCAGC ATGTTGGTAG CTCCTTACGT CTCTAGACAT GCCCATGAGT TTTGTGTCCG

FIGURE 8

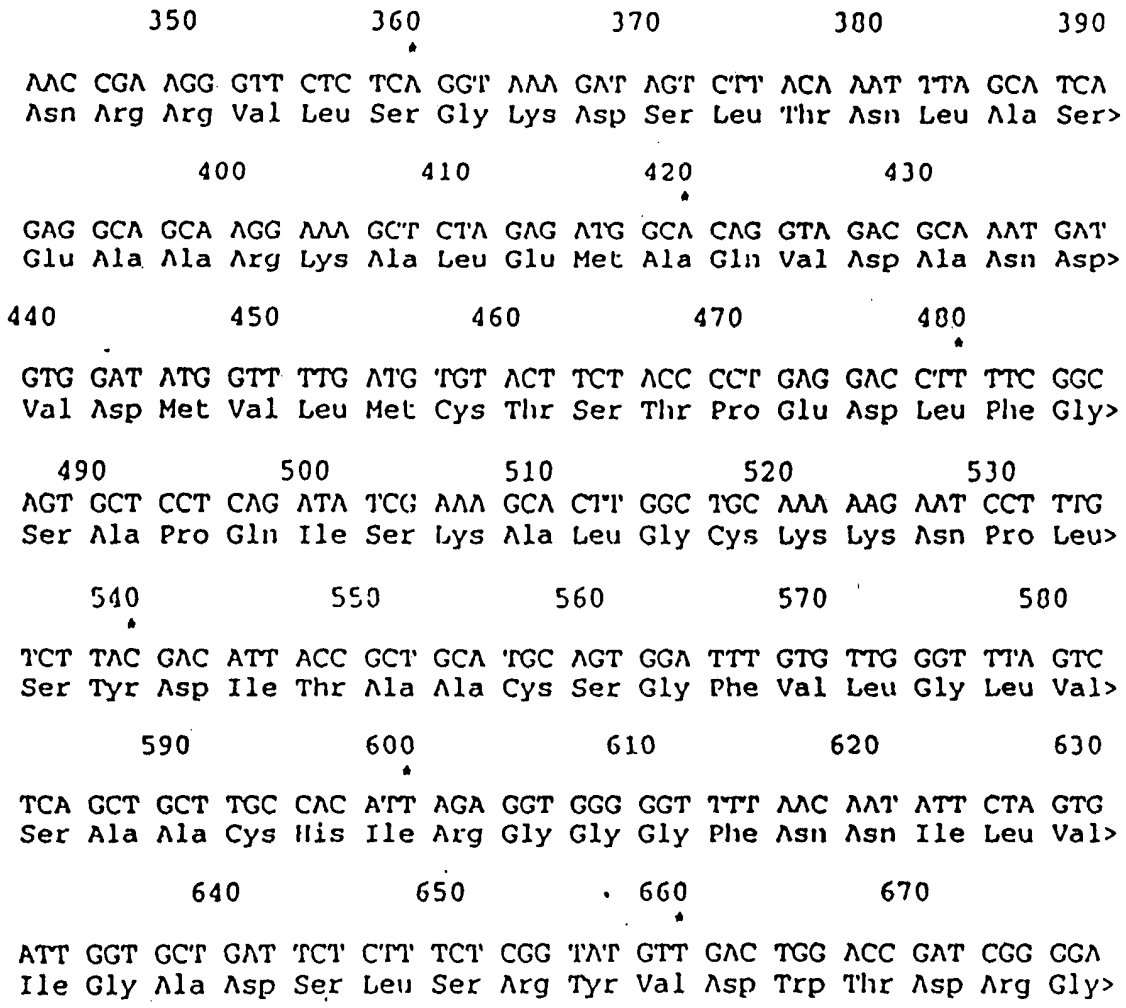
```
      2050        2060        2070        2080        2090        2100
GAGCTTTAGT CGGAACCATG ACGGATTGAG TACTCATGGC GACACTTGAT ATACTCCTTG

      2110        2120        2130        2140        2150        2160
CTAGAATTGT TGGTAGAGCA ATATTCATTA TCTCATATTT TTTTTTTCTC TGAAATCTCC

      2170        2180        2190        2200        2210        2220
CTCCTTGCAA TAGTTGTACT TTCGAGCTTT TCATCGAGTC AGTGAAGAAG AGAACAAAGC

      2230        2240        2250        2260        2270        2280
TGTTAACTCG GGCACGTAGT AACCATTTGC CCTTTGTTTT GCTCTCTATT TCATCACCGT

      2290        2300        2310        2320        2330        2340
TTTGTGGTTT TAAAATTTGT AAAACTAGAA GACTGGTTTA GATTGGTTTG TTTTCTCAAA

      2350        2360        2370
AAAAAAAAAA AAGGGCGGCC GCTCTAGAGG ATCC
```

FIGURE 8
5/5

Sequence Range: 1 to 1580

```
          10          20          30          40          50
CCTGAATCGG ATTCAAGAGA GAGTTTCGTT GCTGGG ATG GCG AAT GCA TCT GGG
                                        Met Ala Asn Ala Ser Gly>

      60          70          80          90          100
      *
TTT CTG GGT TCT TCA GTT CCT GCC CTG AGA AGG GCA ACT CAG CAT TCG
Phe Leu Gly Ser Ser Val Pro Ala Leu Arg Arg Ala Thr Gln His Ser>

        110         120         130         140         150
                    *
ATT TCA TCG TCT CGT GGA TCT TCC TCG GAG TTT GTC TCC AAA AGG GTG
Ile Ser Ser Ser Arg Gly Ser Ser Ser Glu Phe Val Ser Lys Arg Val>

           160         170         180         190
                                   *
TTT TGC TGT AGT GCC GTT CAG GAT TCT GAC AGG CAG TCT TTG GGT GAT
Phe Cys Cys Ser Ala Val Gln Asp Ser Asp Arg Gln Ser Leu Gly Asp>

200         210         220         230         240
                                                *
TCT CGC TCG CCG AGG CTT GTG AGT AGA GGA TGC AAA TTA ATT GGA TCT
Ser Arg Ser Pro Arg Leu Val Ser Arg Gly Cys Lys Leu Ile Gly Ser>

  250         260         270         280         290
GGT TCT GCT ATA CCA GCT CTT CAA GTC TCA AAT GAT GAT CTT GCT AAA
Gly Ser Ala Ile Pro Ala Leu Gln Val Ser Asn Asp Asp Leu Ala Lys>

     300         310         320         330         340
     *
ATT GTC GAC ACC AAT GAT GAA TGG ATT ACT GTC CGA ACG GGG ATC CGC
Ile Val Asp Thr Asn Asp Glu Trp Ile Thr Val Arg Thr Gly Ile Arg>
```

FIGURE 9


350 360 370 380 390
AAC CGA AGG GTT CTC TCA GGT AAA GAT AGT CTT ACA AAT TTA GCA TCA
Asn Arg Arg Val Leu Ser Gly Lys Asp Ser Leu Thr Asn Leu Ala Ser>
400 410 420 430
GAG GCA GCA AGG AAA GCT CTA GAG ATG GCA CAG GTA GAC GCA AAT GAT
Glu Ala Ala Arg Lys Ala Leu Glu Met Ala Gln Val Asp Ala Asn Asp>
440 450 460 470 480
GTG GAT ATG GTT TTG ATG TGT ACT TCT ACC CCT GAG GAC CTT TTC GGC
Val Asp Met Val Leu Met Cys Thr Ser Thr Pro Glu Asp Leu Phe Gly>
490 500 510 520 530
AGT GCT CCT CAG ATA TCG AAA GCA CTT GGC TGC AAA AAG AAT CCT TTG
Ser Ala Pro Gln Ile Ser Lys Ala Leu Gly Cys Lys Lys Asn Pro Leu>
540 550 560 570 580
TCT TAC GAC ATT ACC GCT GCA TGC AGT GGA TTT GTG TTG GGT TTA GTC
Ser Tyr Asp Ile Thr Ala Ala Cys Ser Gly Phe Val Leu Gly Leu Val>
590 600 610 620 630
TCA GCT GCT TGC CAC ATT AGA GGT GGG GGT TTT AAC AAT ATT CTA GTG
Ser Ala Ala Cys His Ile Arg Gly Gly Gly Phe Asn Asn Ile Leu Val>
640 650 660 670
ATT GGT GCT GAT TCT CTT TCT CGG TAT GTT GAC TGG ACC GAT CGG GGA
Ile Gly Ala Asp Ser Leu Ser Arg Tyr Val Asp Trp Thr Asp Arg Gly>
FIGURE 9

```
680          690          700          710          720
                                                     *
ACA TGT ATT CTC TTT GGA GAT GCT GCT GGA GCT GTA GTG GTG CAG TCA
Thr Cys Ile Leu Phe Gly Asp Ala Ala Gly Ala Val Val Val Gln Ser>

  730          740          750          760          770
TGT GAT GCT GAG GAA GAT GGG CTC TTT GCT TTT GAT TTG CAT AGC GAT
Cys Asp Ala Glu Glu Asp Gly Leu Phe Ala Phe Asp Leu His Ser Asp>

    780          790          800          810          820
     *
GGA GAT GGG CAA AGG CAT CTA AAA GCT GCA ATC AAA GAA GAT GAA GTT
Gly Asp Gly Gln Arg His Leu Lys Ala Ala Ile Lys Glu Asp Glu Val>

       830          840          850          860          870
                    *
GAT AAA GCC CTG GGA CAT AAT GGG TCC ATC AGA GAT TTT CCA CCA AGG
Asp Lys Ala Leu Gly His Asn Gly Ser Ile Arg Asp Phe Pro Pro Arg>

          880          890          900          910
                                    *
CGT TCT TCA TAC TCT TGC ATC CAA ATG AAC GGT AAA GAG GTA TTC CGC
Arg Ser Ser Tyr Ser Cys Ile Gln Met Asn Gly Lys Glu Val Phe Arg>

920          930          940          950          960
                                                     *
TTT GCT TGC CGC TCT GTG CCT CAG TCA ATC GAA TCA GCA CTT GGA AAG
Phe Ala Cys Arg Ser Val Pro Gln Ser Ile Glu Ser Ala Leu Gly Lys>

  970          980          990          1000         1010
GCC GGT CTT AAT GGA TCC AAC ATC GAC TGG TTG CTG CTT CAT CAG GCA
Ala Gly Leu Asn Gly Ser Asn Ile Asp Trp Leu Leu Leu His Gln Ala>
```

FIGURE 9

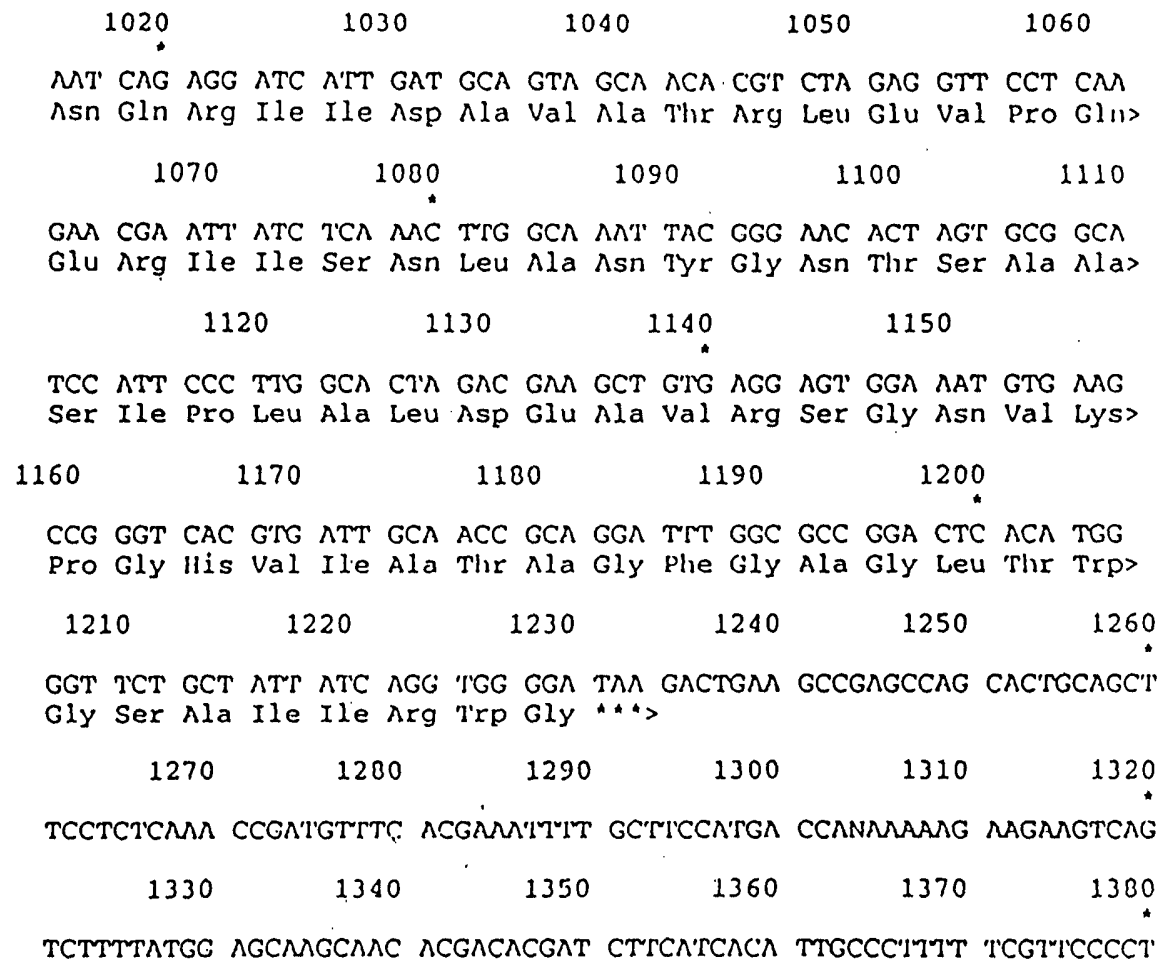

1020 1030 1040 1050 1060
AAT CAG AGG ATC ATT GAT GCA GTA GCA ACA CGT CTA GAG GTT CCT CAA
Asn Gln Arg Ile Ile Asp Ala Val Ala Thr Arg Leu Glu Val Pro Gln>
1070 1080 1090 1100 1110
GAA CGA ATT ATC TCA AAC TTG GCA AAT TAC GGG AAC ACT AGT GCG GCA
Glu Arg Ile Ile Ser Asn Leu Ala Asn Tyr Gly Asn Thr Ser Ala Ala>
1120 1130 1140 1150
TCC ATT CCC TTG GCA CTA GAC GAA GCT GTG AGG AGT GGA AAT GTG AAG
Ser Ile Pro Leu Ala Leu Asp Glu Ala Val Arg Ser Gly Asn Val Lys>
1160 1170 1180 1190 1200
CCG GGT CAC GTG ATT GCA ACC GCA GGA TTT GGC GCC GGA CTC ACA TGG
Pro Gly His Val Ile Ala Thr Ala Gly Phe Gly Ala Gly Leu Thr Trp>
1210 1220 1230 1240 1250 1260
GGT TCT GCT ATT ATC AGG TGG GGA TAA GACTGAA GCCGAGCCAG CACTGCAGCT
Gly Ser Ala Ile Ile Arg Trp Gly ***>
1270 1280 1290 1300 1310 1320
TCCTCTCAAA CCGATGTTTC ACGAAATTTT GCTTCCATGA CCANAAAAAG AAGAAGTCAG
1330 1340 1350 1360 1370 1380
TCTTTTATGG AGCAAGCAAC ACGACACGAT CTTCATCACA TTGCCCTTTT TCGTTCCCCT

FIGURE 9

1390 1400 1410 1420 1430 1440

TTTCCATTAG TTTGATGATT TTGCTGACAA TACAATACCC ATAGTTTCTT TTGTCCCCAA

1450 1460 1470 1480 1490 1500

TAAGTTATTT GTTTCTTGTT TAATTGTTCA GCTTTTTACTT CATTTTGTCT CGGGACATTG

1510 1520 1530 1540 1550 1560

GAGATGACAG CATAAACATC ATGTTTATAT TTTGCTAAAA AAAAAAAAAA AAAAAAAAAA

1570 1580

AAAAAAAAAA AAAAAAAAAA

FIGURE 9

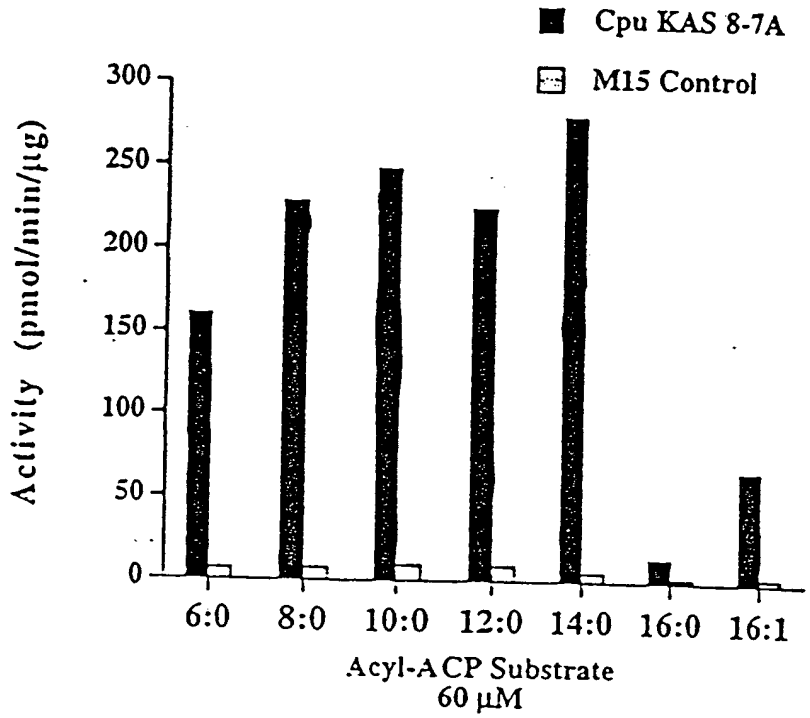

Cpu KAS 8-7A
M15 Control
Activity (pmol/min/µg)
300
250
200
150
100
50
0
6:0
8:0
10:0
12:0
14:0
16:0
16:1
Acyl-ACP Substrate
60 µM

FIGURE 10

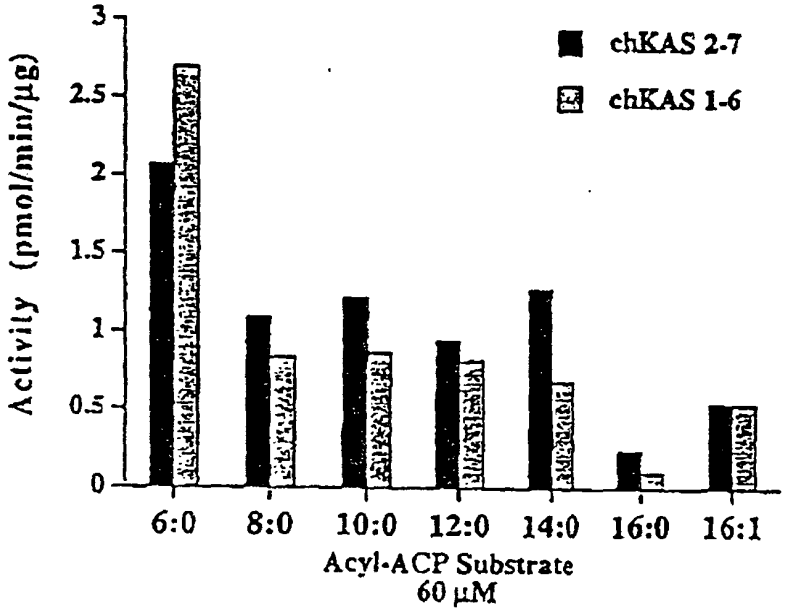

Activity (pmol/min/µg)
3
2.5
2
1.5
1
0.5
0
chKAS 2-7
chKAS 1-6
6:0
8:0
10:0
12:0
14:0
16:0
16:1
Acyl-ACP Substrate
60 µM

FIGURE 11

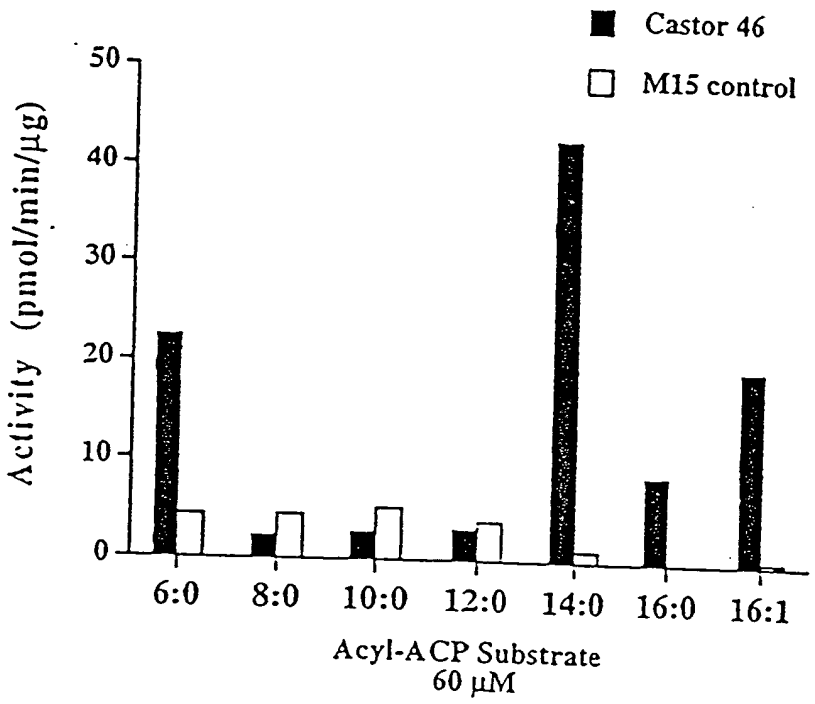
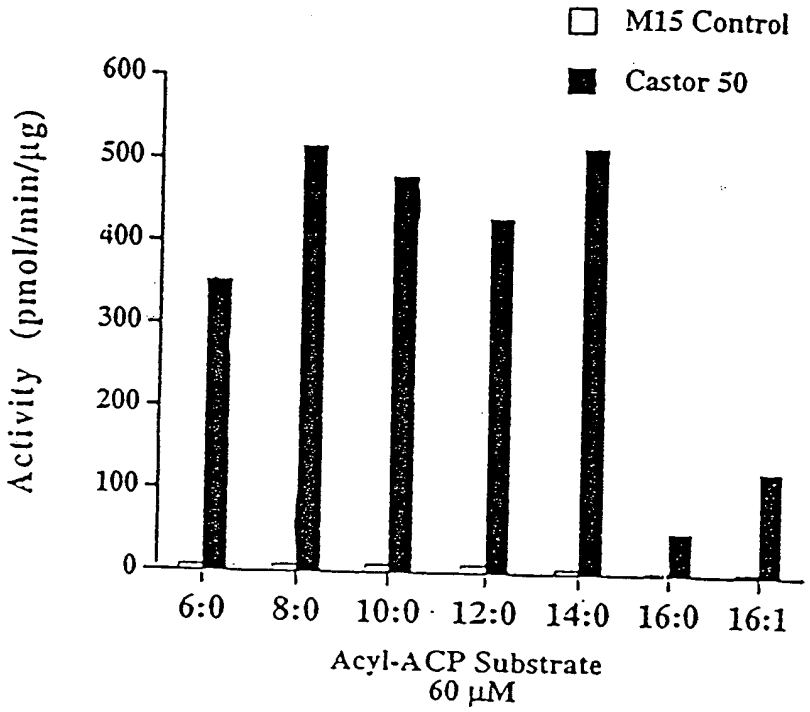

Castor 46
M15 control
Activity (pmol/min/µg)
50
40
30
20
10
0
6:0
8:0
10:0
12:0
14:0
16:0
16:1
Acyl-ACP Substrate
60 µM

FIGURE 12



E328013-28

FIGURE 13

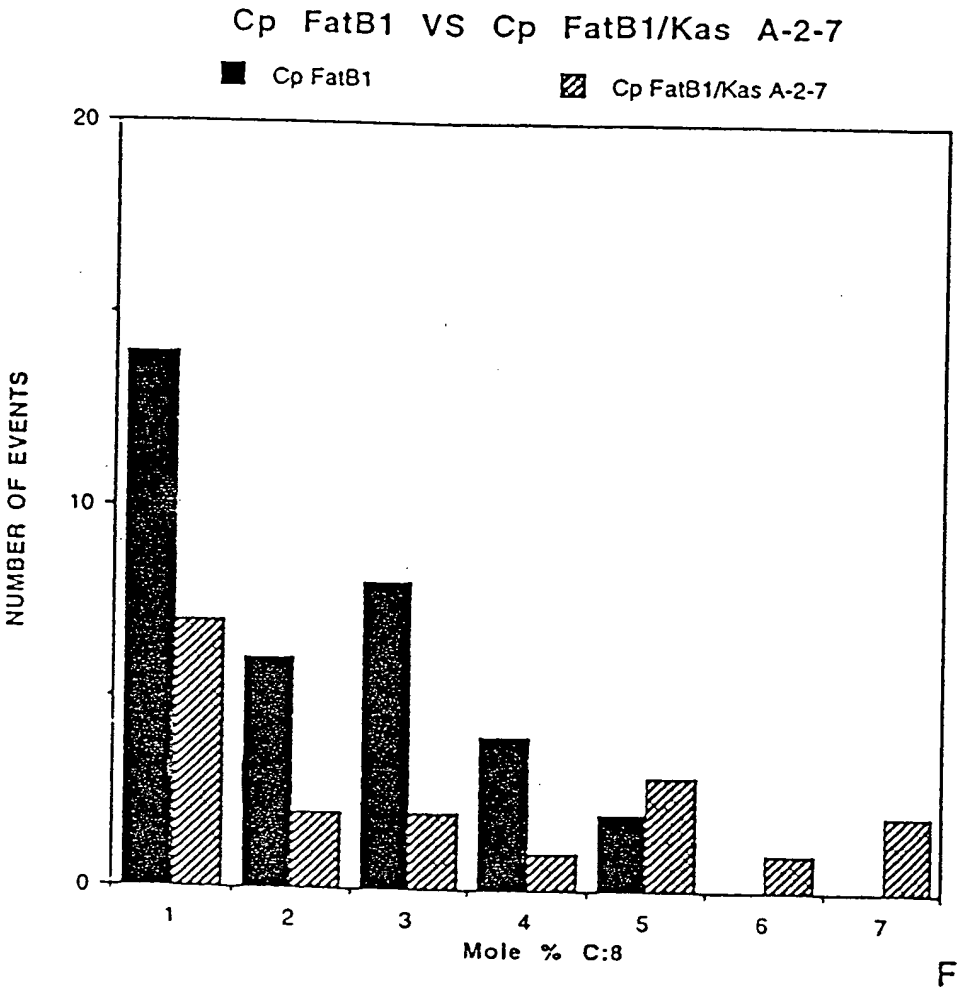

Cp FatB1 VS Cp FatB1/Kas A-2-7
Cp FatB1
Cp FatB1/Kas A-2-7
NUMBER OF EVENTS
20
10
0
1
2
3
4
5
6
7
Mole % C:8

FIGURE 14

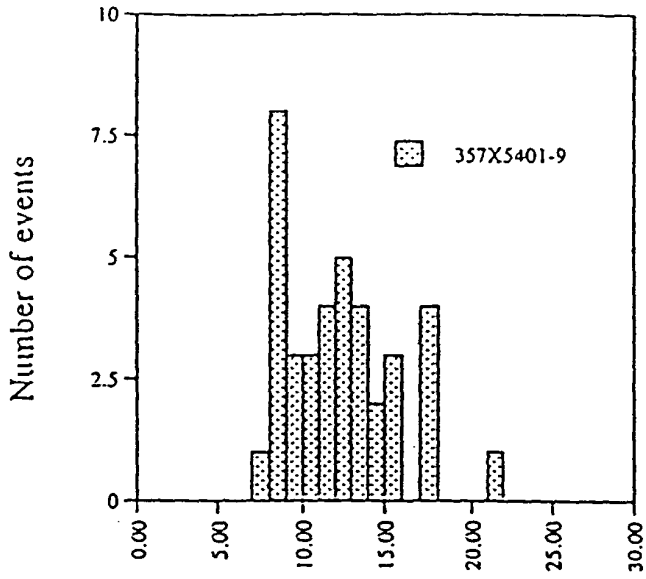


FIGURE 15A

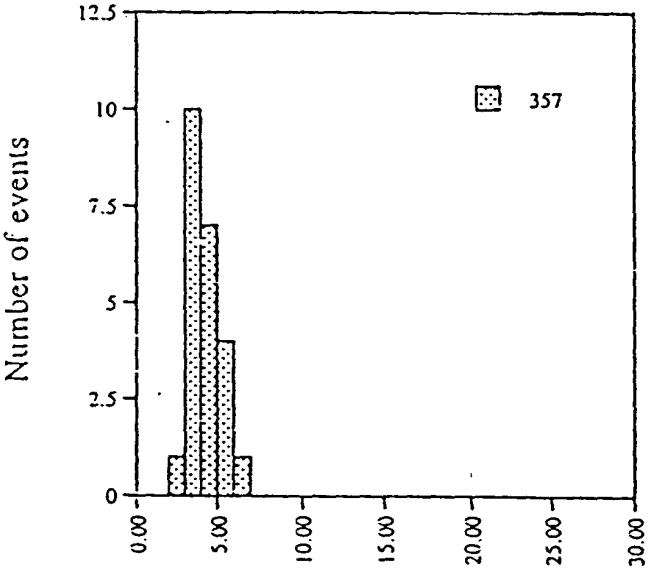


FIGURE 15B

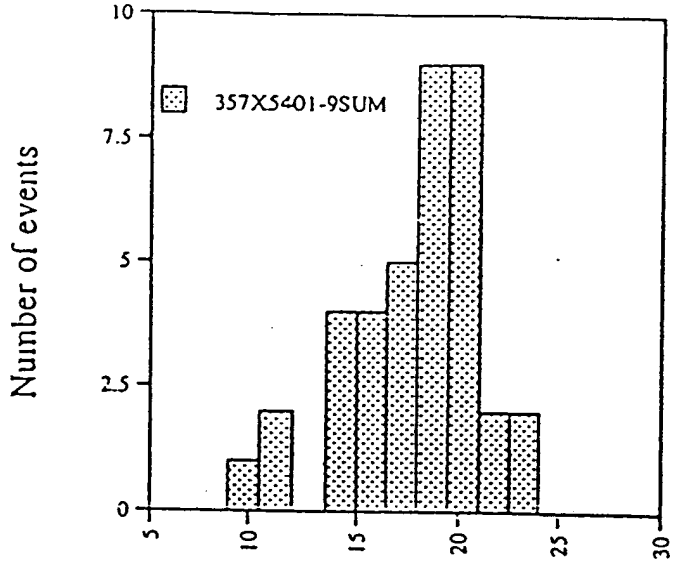


FIGURE 16A

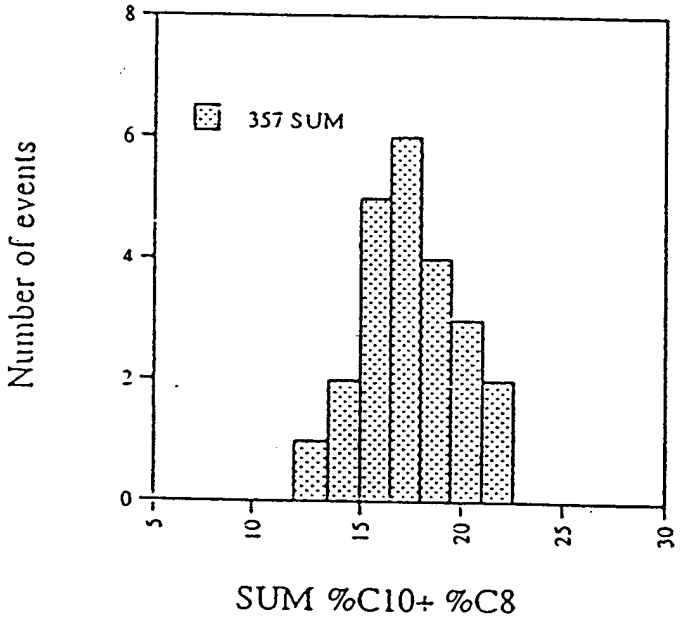


FIGURE 16B

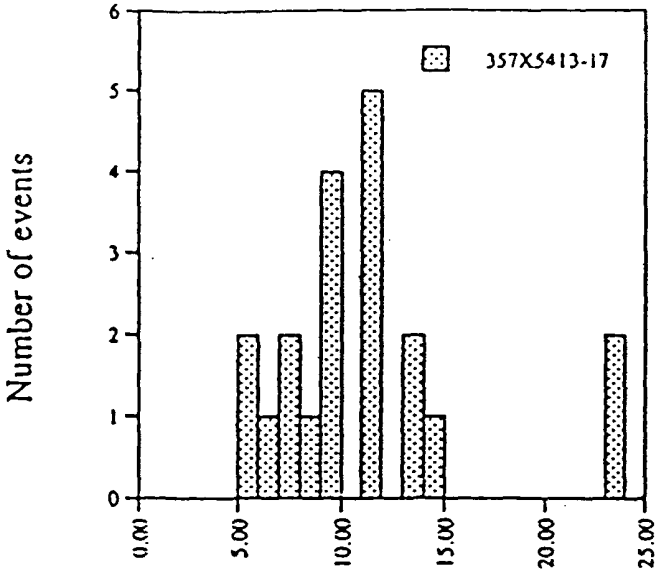


FIGURE 17A

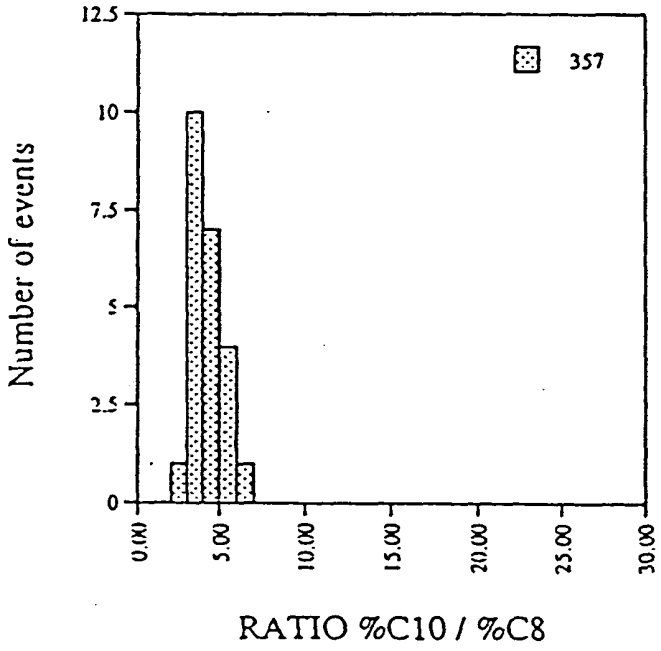


FIGURE 17B

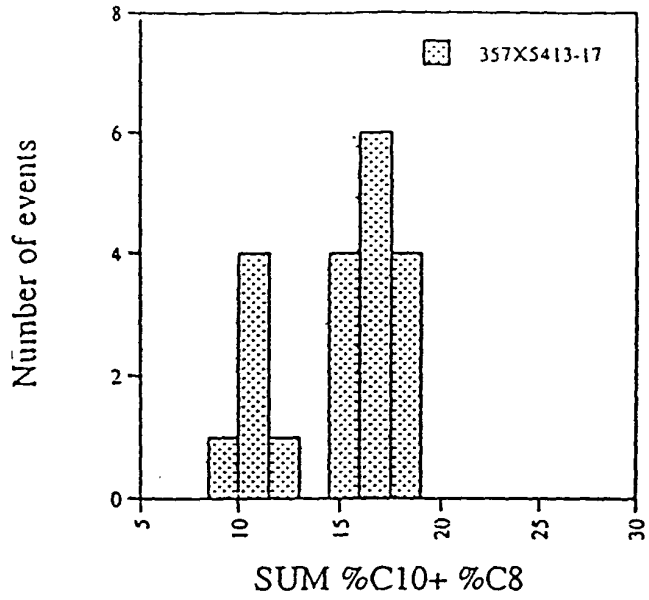


FIGURE 18A

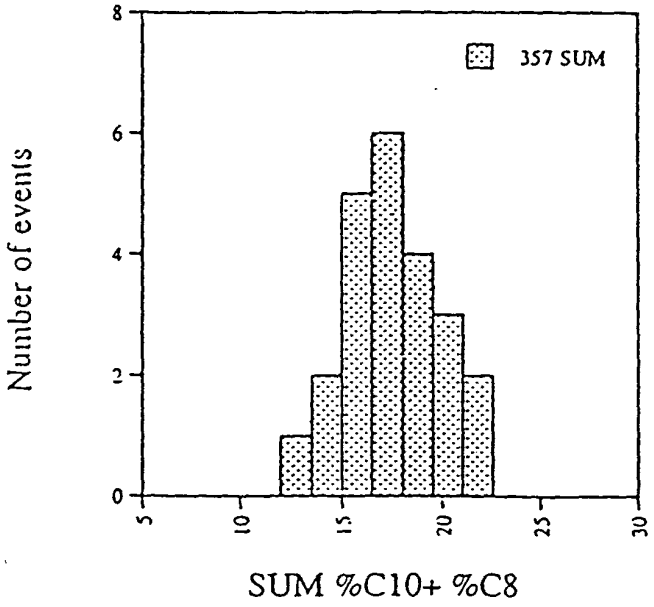


FIGURE 18B

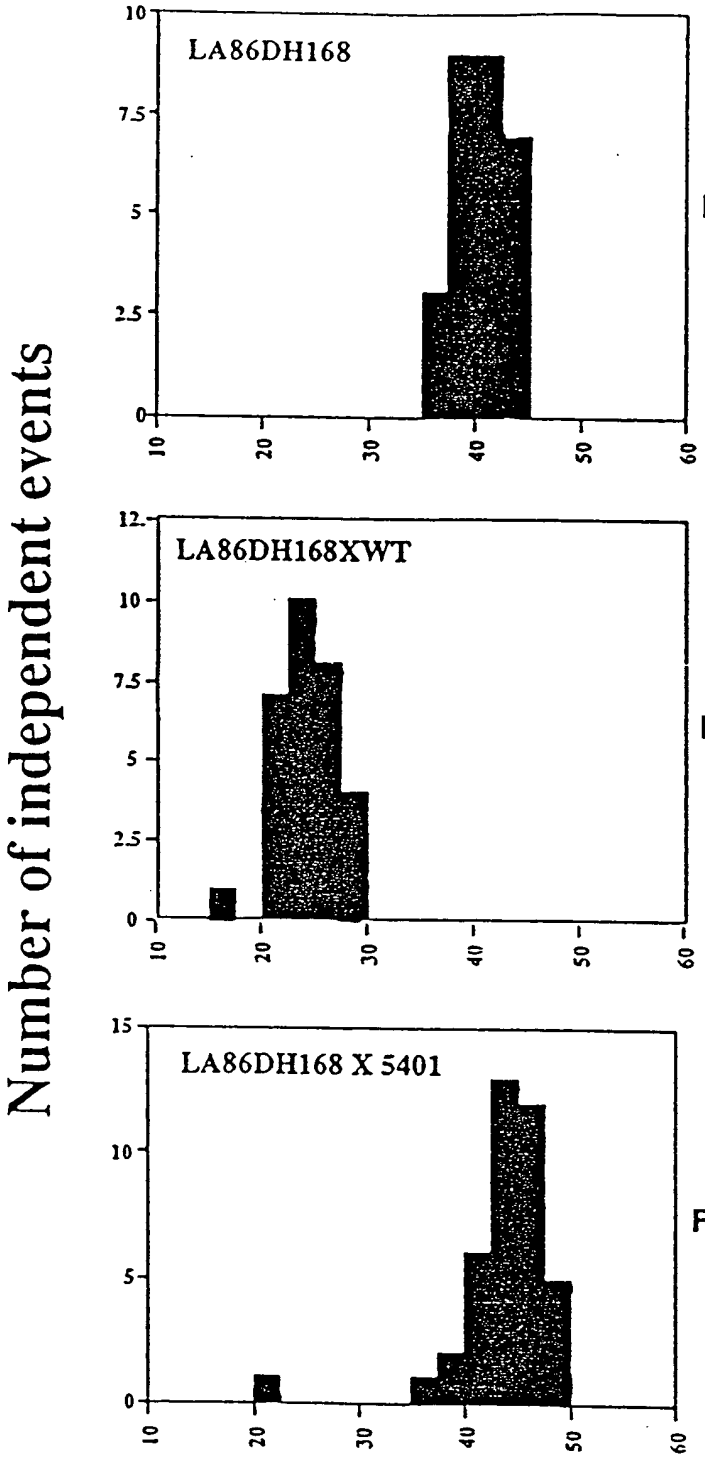


FIGURE 19A

FIGURE 19B

FIGURE 19BC

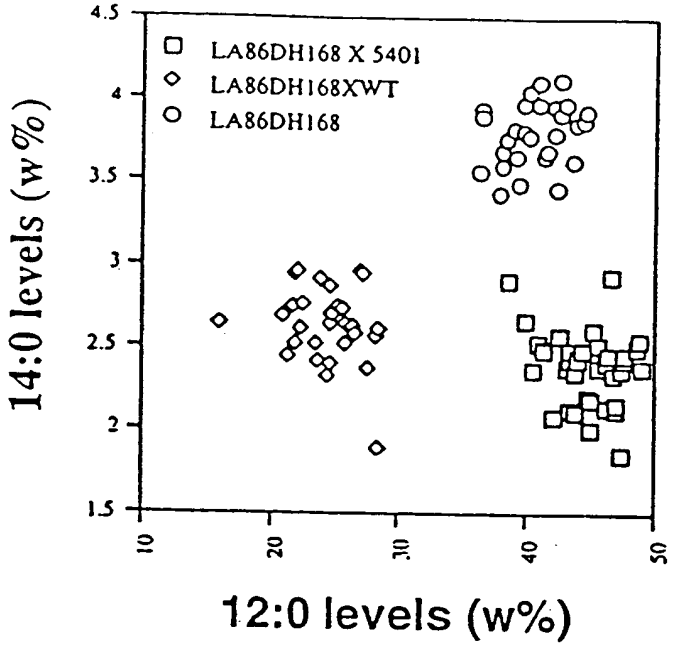

LA86DH168 X 5401
LA86DH168XWT
LA86DH168
14:0 levels (w%)
12:0 levels (w%)
4.5
4
3.5
3
2.5
2
1.5
10
20
30
40
50

FIGURE 20

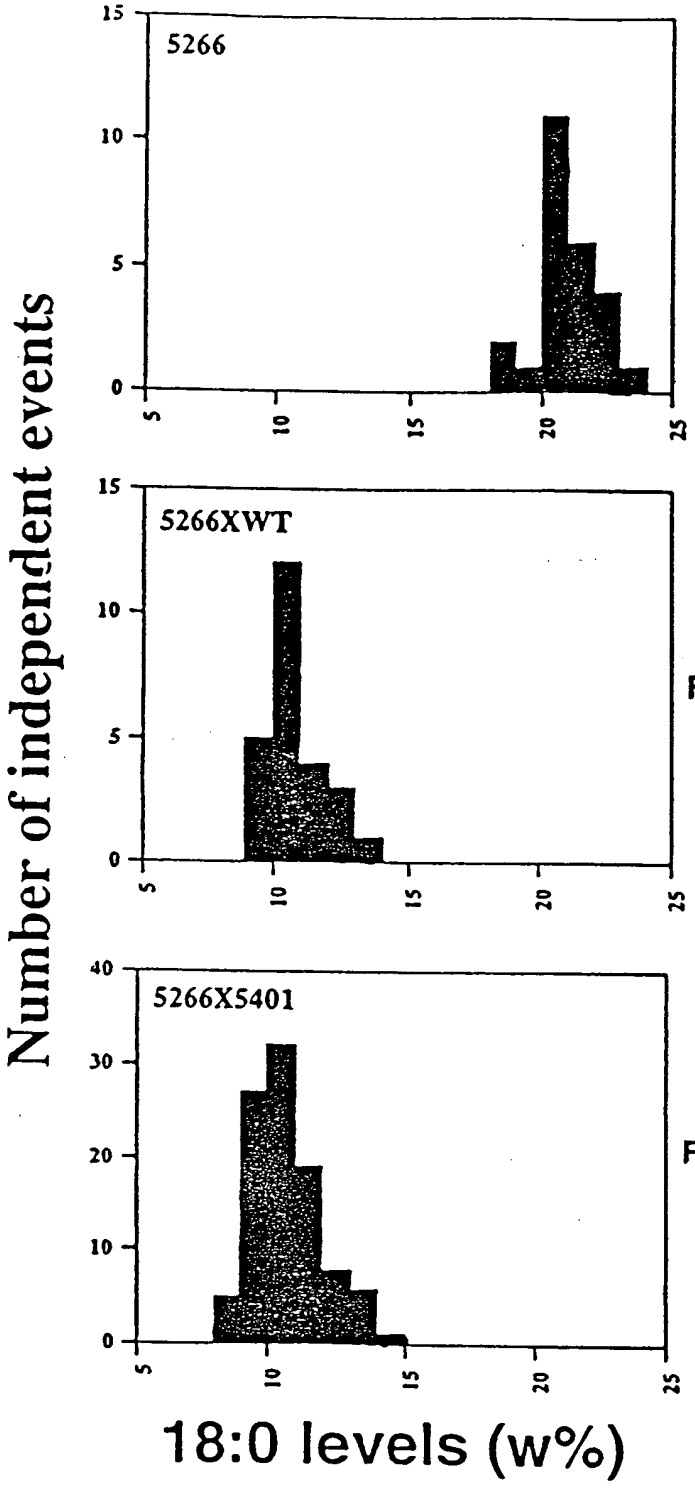


FIGURE 21A

FIGURE 21B

FIGURE 21C

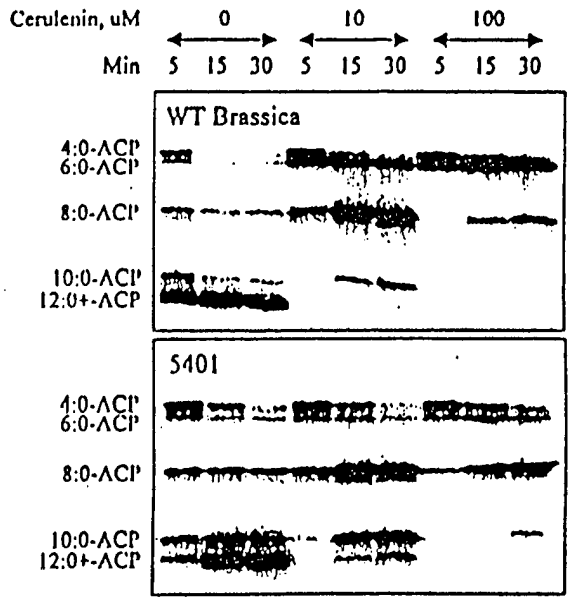

Cerulenin, uM
0
10
100
Min
5 15 30 5 15 30 5 15 30
WT Brassica
4:0-ACP
6:0-ACP
8:0-ACP
10:0-ACP
12:0+-ACP
5401
4:0-ACP
6:0-ACP
8:0-ACP
10:0-ACP
12:0+-ACP

FIGURE 22